

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:49:31 : Search time 13 Seconds  
(without alignments)  
56.367 Million cell updates/sec

Title: US-09-720-828A-4

Perfect score: 147

Sequence: 1 APTSSSTKKTQLEHLDDLMWLINGINN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:.\*  
2: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:.\*  
3: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:.\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:.\*  
5: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:.\*  
6: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	31	4	US-09-116-594-2
2	147	100.0	50	1	US-08-127-351-13
3	147	100.0	50	1	US-08-480-367B-13
4	147	100.0	50	1	US-08-487-231A-13
5	147	100.0	50	1	US-08-480-370-13
6	147	100.0	88	4	US-08-817-787-15
7	147	100.0	96	4	US-08-160-376A-5
8	147	100.0	96	1	US-08-389-487-8
9	147	100.0	133	1	US-07-800-366-1
10	147	100.0	133	1	US-08-354-456A-5
11	147	100.0	133	1	US-08-225-224-3
12	147	100.0	133	1	US-08-318-193-89
13	147	100.0	133	1	US-08-284-393B-1
14	147	100.0	133	1	US-08-284-393B-2
15	147	100.0	133	1	US-08-284-393B-3
16	147	100.0	133	1	US-08-734-471-1
17	147	100.0	133	1	US-08-722-258-3
18	147	100.0	133	4	US-08-817-787-13
19	147	100.0	133	4	US-09-310-026-1
20	147	100.0	133	5	PCR-US95-04468-3
21	147	100.0	133	5	PCR-US95-08950-1
22	147	100.0	133	5	PCR-US95-08950-2
23	147	100.0	133	5	PCR-US95-08950-3
24	147	100.0	133	6	5210029-1
25	147	100.0	133	6	5256769-1
26	147	100.0	133	6	5464939-2
27	147	100.0	134	6	5496924-55

28	147	100.0	153	3	US-09-012-366-3	Sequence 3, App1
29	147	100.0	153	4	US-08-759-628-8	Sequence 8, App1
30	147	100.0	153	4	US-09-522-217-111	Sequence 111, App
31	147	100.0	153	6	5314995-7	Patent No. 5314995
32	147	100.0	157	4	US-08-818-562-2	Sequence 2, App1
33	147	100.0	478	3	US-08-155-888-2	Sequence 2, App1
34	147	100.0	504	1	US-07-932-915-2	Sequence 2, App1
35	147	100.0	504	3	PCR-US91-05826-2	Sequence 2, App1
36	144	98.0	251	5	US-08-875-811-59	Sequence 59, App1
37	144	98.0	254	3	US-08-875-811-61	Sequence 61, App1
38	143	97.3	133	3	US-08-354-456A-6	Sequence 3, App1
39	132.5	90.1	127	3	US-08-806-121B-3	Sequence 3, App1
40	102	69.4	141	4	US-08-930-917A-18	Sequence 18, App1
41	79	53.7	135	2	US-08-383-621-5	Sequence 5, App1
42	79	53.7	135	3	US-08-459-906-5	Sequence 5, App1
43	79	53.7	1098	1	US-07-777-715-7	Sequence 7, App1
44	79	53.7	1098	1	US-08-170-126-2	Sequence 2, App1
45	79	53.7	1098	3	US-08-954-418-2	Sequence 2, App1

## ALIGNMENTS

RESULT 1  
US-09-116-594-2

Sequence 2, Application US/09116594

Patent No. 618785

GENERAL INFORMATION:

APPLICANT: THEZE, Jacques

APPLICANT: ECKENBERG, Ralph

APPLICANT: MOREAU, Jean-Louis

APPLICANT: MAZIE, Jean-Claude

TITLE OF INVENTION: BIOLOGICAL APPLICATIONS OF NEW PEPTIDES OF IL-2 AND

FILE REFERENCE: 0660-0134-0

CURRENT FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 31

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:peptide

US-09-116-594-2

Query Match

Best Local Similarity 100.0%; Score 147; DB 4; Length 31;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 APTSSSTKKTQLEHLDDLMWLINGINN 31

RESULT 2  
US-08-127-351-13

Sequence 13, Application US/08127351

Patent No. 5449761

GENERAL INFORMATION:

APPLICANT: BELINKA JR, BENJAMIN A.

APPLICANT: COUGHLIN, DANIEL J.

APPLICANT: ALVAREZ, VERNON L.

TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE

TITLE OF INVENTION: CONSTRUCTS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &

ADDRESSEE: NEUSTADT,

ADDRESSEE: P.C.

ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400

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? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/127,351
? FILING DATE: 28-SEP-1993
? CLASSIFICATION: 534
? ATTORNEY/AGENT INFORMATION:
? NAME: Villacorta, Gilberto M.
? REGISTRATION NUMBER: 34,038
? REFERENCE/DOCKET NUMBER: 4980-004-44
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 413-3000
? TELEFAX: (703) 413-2220
? TELEX: 248855 OPAT UR
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 50 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: peptide
? US-08-127-351-13

Query Match
Best Local Similarity 100.0%; Score 147; DB 1; Length 50;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30
DB 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30

RESULT 3
US-08-480-367B-13
? Sequence 13, Application US/08480367B
? Patent No. 5578288
? GENERAL INFORMATION:
? APPLICANT: BELINKA JR, BENJAMIN A.
? APPLICANT: COUGHLIN, DANIEL J.
? APPLICANT: ALVAREZ, VERNON L.
? APPLICANT: WOOD, RICHARD
? TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
? NUMBER OF SEQUENCES: 56
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
? STREET: 99 Canal Center Plaza, Suite 300
? CITY: Alexandria
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22314
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/480,367B
? FILING DATE: 07-06-95
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Villacorta, Gilberto M.
? REGISTRATION NUMBER: 34,038
? REFERENCE/DOCKET NUMBER: 2654-002A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 684-1111
? TELEFAX: (703) 684-1124

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? TELEX:
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 50 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: peptide
? US-08-480-367B-13

Query Match
Best Local Similarity 100.0%; Score 147; DB 1; Length 50;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30
DB 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30

RESULT 4
US-08-487-221A-13
? Sequence 13, Application US/08487221A
? Patent No. 5593656
? GENERAL INFORMATION:
? APPLICANT: BELINKA JR, BENJAMIN A.
? APPLICANT: COUGHLIN, DANIEL J.
? APPLICANT: ALVAREZ, VERNON L.
? APPLICANT: WOOD, RICHARD
? TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
? NUMBER OF SEQUENCES: 56
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
? STREET: 1755 S. Jefferson Davis Highway, Suite 400
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/487,221A
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/127,351
? FILING DATE: 28-SEP-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Villacorta, Gilberto M.
? REGISTRATION NUMBER: 34,038
? REFERENCE/DOCKET NUMBER: 4980-004-44
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 413-3000
? TELEFAX: (703) 413-2220
? TELEX: 248855 OPAT UR
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 50 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: peptide
? US-08-487-221A-13

Query Match
Best Local Similarity 100.0%; Score 147; DB 1; Length 50;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30
DB 1 APTSSSTKTKTQLQLEHLLLDLQMLNGINN 30

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RESULT 5  
US-08-480-370-13  
; Sequence 13, Application US/08480370  
; Patent No. 5609847  
; GENERAL INFORMATION:  
; APPLICANT: BELINKA JR, BENJAMIN A.  
; APPLICANT: COUGHLIN, DANIEL J.  
; APPLICANT: ALVAREZ, VERNON L.  
; APPLICANT: WOOD, RICHARD  
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
; TITLE OF INVENTION: CONSTRUCTS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,370  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/127,351  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-004-44  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-480-370-13  
Query Match 100.0%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.4e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 APTSSSTKTQLEHLHLDLQMLNGINN 30  
DB 1 APTSSSTKTQLEHLHLDLQMLNGINN 30  
RESULT 6  
US-08-817-787-15  
; Sequence 15, Application US/08817787  
; Patent No. 6294353  
; GENERAL INFORMATION:  
; APPLICANT: Pack, Peter  
; APPLICANT: Lupas, Andrei  
; TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF  
; TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,787  
FILING DATE: 23-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04117  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94 11 6558.1  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9000  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 88 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-817-787-15  
Query Match 100.0%; Score 147; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 6.8e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 APTSSSTKTQLEHLHLDLQMLNGINN 30  
DB 3 APTSSSTKTQLEHLHLDLQMLNGINN 32  
RESULT 7  
US-08-160-376A-5  
; Sequence 5, Application US/08160376A  
; Patent No. 5473049  
; GENERAL INFORMATION:  
; APPLICANT: Obermeyer, Ranier  
; APPLICANT: Gerl, Martin  
; APPLICANT: Ludwig, Jurgen  
; APPLICANT: Sabel, Walter  
; TITLE OF INVENTION: Process For Obtaining Proinsulin  
; TITLE OF INVENTION: Possessing Correctly Linked  
; Cysteine Bridges  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth A. Genoni, Esq.  
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500  
; CITY: Somerville  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 08876-1258  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 386  
OPERATING SYSTEM: WINDOWS 3.1  
SOFTWARE: WORDPERECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/160,376A  
FILING DATE: December 1, 1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara V. Maurer, Esq.
REGISTRATION NUMBER: 31,287
REFERENCE/DOCKET NUMBER: HOE 92/F 384
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 Amino Acids
TYPE: Amino Acid (AA)
TOPOLOGY: not relevant
US-08-160-376A-5

Query Match          100.0%; Score 147; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 7,6e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLEHLLDLMILNGINN 30
Db 2 APTSSSTKKTQLEHLLDLMILNGINN 31

RESULT 8
US-08-389-487-8
Sequence 8, Application US/08389487
Patent No. 5663291
GENERAL INFORMATION:
APPLICANT: Obermeier, Rainer
APPLICANT: Gerl, Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process for obtaining Insulin Having
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,487
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1424-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-389-487-8

Query Match          100.0%; Score 147; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 7,6e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 APTSSSTKKTQLEHLLDLMILNGINN 30
Db 2 APTSSSTKKTQLEHLLDLMILNGINN 31

RESULT 9
US-07-800-366-1
Sequence 1, Application US/07800366
Patent No. 5250296
GENERAL INFORMATION:
APPLICANT: OOTSU, Koichihiro
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSER: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/800,366
FILING DATE: 19911127
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Caslie, Donald R
REGISTRATION NUMBER: 24,220
REFERENCE/DOCKET NUMBER: 41417(281)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-800-366-1

Query Match          100.0%; Score 147; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLEHLLDLMILNGINN 30
Db 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 10
US-08-354-456A-5
Sequence 5, Application US/08354456A
Patent No. 5567611
GENERAL INFORMATION:
APPLICANT: Ralph, Peter
APPLICANT: Martin, George
APPLICANT: Platek, Michael
APPLICANT: Larrick, James W.
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville

```

STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,456A  
CLASSIFICATION: 435  
FILING DATE: 12-DEC-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/995,338  
FILING DATE: 21-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McGarrigle Jr., Philip L.  
REGISTRATION NUMBER: 31,395  
REFERENCE/DOCKET NUMBER: 750,003/32387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2718  
TELEFAX: (510) 655-3542  
TELEX: R/A  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-456A-5

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLHLLDQMLNGINN 30  
Db 1 APTSSSTKKTQLEHLHLLDQMLNGINN 30

RESULT 11  
US-08-225-224-3  
Sequence 3, Application US/08225224  
Patent No. 5635599  
GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..133  
OTHER INFORMATION: /label= IL2  
US-08-225-224-3

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLHLLDQMLNGINN 30  
Db 1 APTSSSTKKTQLEHLHLLDQMLNGINN 30

RESULT 12  
US-08-318-193-89  
Sequence 89, Application US/08318193  
Patent No. 5641663  
GENERAL INFORMATION:  
APPLICANT: GARVIN, Robert T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION  
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY  
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314  
FILING DATE:  
APPLICATION NUMBER: US 07/224,566  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-193-89

Query Match 100.0%; Score 147; DB 1; Length 133;

Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTOLLEHLLDLMINGINN 30  
|||||  
Db 1 APTSSSTKTKTOLLEHLLDLMINGINN 30

## RESULT 13

US-08-284-393B-1  
Sequence 1, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-1

Query Match 100.0%; Score 147; DB 1; length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTOLLEHLLDLMINGINN 30  
|||||  
Db 1 APTSSSTKTKTOLLEHLLDLMINGINN 30

## RESULT 14

US-08-284-393B-2  
Sequence 2, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA

ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-2

Query Match 100.0%; Score 147; DB 1; length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTOLLEHLLDLMINGINN 30  
|||||  
Db 1 APTSSSTKTKTOLLEHLLDLMINGINN 30

## RESULT 15

US-08-284-393B-3  
Sequence 3, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: peptide  
US-08-284-393B-3

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1, 1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQIQLEHLLLDLQMLINGINN 30  
|||||  
DB 1 APTSSSTKKTQIQLEHLLLDLQMLINGINN 30

Search completed: October 25, 2002, 15:53:05  
Job time : 13 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:43:41 ; Search time 31 Seconds

(without alignments)  
111.074 Million cell updates/sec

Title: US-09-720-828a-2

Perfect score: 152

Sequence: 1 MAPSSSTKKTQLQLEHLIDQMLNGINN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	31	21	AAV51597
2	152	100.0	58	12	AAK1015
3	152	100.0	60	11	AAK0638
4	152	100.0	60	15	AAK48245
5	152	100.0	96	15	AAK68899
6	152	100.0	96	16	AAK78662
7	152	100.0	133	13	AAK22595
8	152	100.0	134	5	AAK40050
9	152	100.0	134	6	AAK50053
10	152	100.0	134	6	AAK50855
11	152	100.0	134	7	AAK61102

12	152	100.0	134	8	AAK70585
13	152	100.0	134	11	AAK05267
14	152	100.0	134	11	AAK05266
15	152	100.0	134	11	AAK05240
16	152	100.0	136	20	AAK49917
17	152	100.0	143	15	AAK50932
18	152	100.0	149	11	AAK07265
19	152	100.0	149	11	AAK07266
20	152	100.0	149	11	AAK07267
21	152	100.0	149	11	AAK07269
22	152	100.0	149	11	AAK07148
23	152	100.0	149	11	AAK07149
24	152	100.0	149	11	AAK07150
25	152	100.0	149	11	AAK07261
26	152	100.0	149	11	AAK07262
27	152	100.0	149	11	AAK07263
28	152	100.0	149	11	AAK07264
29	152	100.0	172	10	AAK94809
30	152	100.0	201	11	AAK06839
31	152	100.0	255	6	AAK50305
32	152	100.0	273	6	AAK50087
33	152	100.0	273	6	AAK50310
34	152	100.0	65	10	AAK91032
35	149	98.0	149	11	AAK07146
36	149	98.0	149	11	AAK07268
37	149	98.0	149	11	AAK07255
38	149	98.0	149	11	AAK07256
39	149	98.0	149	11	AAK07257
40	149	98.0	149	11	AAK07258
41	149	98.0	149	11	AAK07259
42	149	98.0	381	22	AAK12707
43	149	98.0	421	17	AAK95055
44	149	98.0	435	12	AAK11273
45	149	98.0	496	17	AAK5058

# ALIGNMENTS

RESULT 1

AAV51597

AAV51597 standard; Protein; 31 AA.

XX

AAV51597;

XX

25-MAY-2000 (first entry)

XX

Human IL-2 derived peptide IP130 #1.

XX

IL-2; Interleukin 2; human; IP130; immunosuppressive; antirheumatic;

KW graft rejection; autoimmune disorder; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

MO200004048-A1.

XX

27-JAN-2000.

XX

16-JUL-1999; 99MO-IB01424.

XX

16-JUL-1998; 98US-0116594.

PR

(INSP ) INST PASTEUR.

PA

These J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;

PI Mazie J;

XX

WPI; 2000-182403/16.

DR N-PSDB; AA288837.

XX

Novel cytokine peptides and antibody for preventing and/or treating

PT undesirable immune reactions e.g. graft rejection and autoimmune

PT disorders

XX  
PS Claim 1; Page 54; 56pp; English.  
XX  
CC This invention describes a novel a peptide, IP130 having 31 (I) or 30  
CC (II) amino acid sequence or its homologous sequence (H) exhibiting the  
CC same activity or binding characteristic. The products of the invention  
CC have immunosuppressive and antirheumatic activity. (I) or (II) is used  
CC for preparing medicament useful to induce IL-2 activity. (A) or a peptide  
CC binding to it is used for inhibiting the activity of IL-2R in treating  
CC conditions related with undesirable immune reactions like graft  
CC rejection, and autoimmune disorders like rheumatoid arthritis. It is also  
CC used for immunofluorescent purification of native or recombinant IL-2  
CC peptides. (V) is also used for preparing medicaments in treating patients  
CC with deficient IL-2 activity. (III) used to prepare antisense  
CC oligonucleotides and ribozymes modulating the expression of IL-2 which  
CC can be used in gene therapy applications. The peptides inhibit or mimics  
CC the binding of helix A of IL-2 to a subunit of an IL-2R and thus produces  
CC a specific interaction. This sequence represents an IP130 peptide  
CC described in the method of the invention.  
XX  
SQ Sequence 31 AA;  
XX  
Query Match 100.0%; Score 152; DB 21; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2,3e-14;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
Db 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
XX  
RESULT 2  
AA11015  
ID AA11015 standard; Peptide; 58 AA.  
XX  
AC AA11015;  
XX  
DT 13-MAY-1991 (first entry)  
XX  
DE Human Interleukin-2-derived stabiliser peptide.  
XX  
KW Interleukin-2; IL-2; gag 24; gp 41; gp 36; HIV detection.  
XX  
OS Homo sapiens.  
XX  
PN EP416673-A.  
XX  
PD 13-MAR-1991.  
XX  
PF 02-AUG-1990; 90EP-0202108.  
XX  
PR 03-AUG-1989; 89CU-0000149.  
XX  
PA (INGE-) CENT ING GENETICA.  
XX  
PI Novoa Perez LI, Machado Lahera JA, Fernandez Maso JR;  
PI Benitez Fuentes JV, Nardicani Diaz RE, Rodriguez Relioso JL;  
PI Estrada Garcia MP, Garcia Suarez J, Herrera Martinez LS;  
XX  
DR WPI: 1991-075197/11.  
DR N-PSDB; AAQ10898.  
XX  
PT Method for expressing heterologous proteins - as fusion protein,  
PT using vector contg. stabilising sequence  
XX  
PS Claim 2; Page 10; 18pp; English.  
XX  
CC The sequence corresponds to the first 58 amino acid residues of  
CC human IL-2. It forms part of a fusion protein, linked to a  
CC heterologous protein. The heterologous protein is preferably gag 24  
CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of  
CC HIV-2. Such fusion proteins can be used to detect antibodies to  
CC these proteins. See also AAQ10899-Q10903.

XX  
SQ Sequence 58 AA;  
XX  
Query Match 100.0%; Score 152; DB 12; Length 58;  
Best Local Similarity 100.0%; Pred. No. 4,6e-14;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
Db 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
XX  
RESULT 3  
AA06838  
ID AA06838 standard; protein; 60 AA.  
XX  
AC AA06838;  
XX  
DT 14-JAN-1991 (first entry)  
XX  
DE Human IL-2 N-terminal transcript of plasmid pT13S.  
XX  
KW Bovine tuberculosis; Interleukin-2; IL-2; plasmid pT13S.  
XX  
OS Mycobacterium bovis.  
XX  
PN JP02195895-A.  
XX  
PD 02-AUG-1990.  
XX  
PF 24-JAN-1989; 89JP-0013270.  
XX  
PR 24-JAN-1989; 89JP-0013270.  
XX  
PA (AJIN ) AJINOMOTO KK.  
XX  
DR WPI: 1990-278851/37.  
DR N-PSDB; AAQ05976.  
XX  
PT BCG bacteria derived immuno:protein MP870 - can be used as  
PT diagnostic agent used to determine bovine tuberculosis.  
XX  
PS Disclosure; Fig 2; 11pp; Japanese.  
XX  
CC Immunoprotein MP870 encoding sequence may be incorporated into  
CC plasmid pT13S with an N-terminal fragment of human IL-2. The plasmid  
CC may be used to transform an expression system giving a fusion  
CC protein which may be used as a diagnostic agent for bovine  
CC tuberculosis infection.  
XX  
SQ Sequence 60 AA;  
XX  
Query Match 100.0%; Score 152; DB 11; Length 60;  
Best Local Similarity 100.0%; Pred. No. 4,8e-14;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
Db 1 MAPSSSTRKTQLEHLLDLDQMILNGINN 31  
XX  
RESULT 4  
AA048245  
ID AA048245 standard; Protein; 60 AA.  
XX  
AC AA048245;  
XX  
DT 12-JUL-1994 (first entry)  
XX  
DE Human Interleukin-2.  
XX  
KW non-coding region; coding region; resonance; interaction; IL-2;  
KW optimisation; degenerate sequence; plasmid pT13Snc; pT9-11;

KW gene expression; regulation; recombinant protein production;  
 KW interleukin-2; interleukin-6.  
 XX Homo sapiens.  
 XX FR2692594-A.  
 XX 24-DEC-1993.  
 XX 22-JUN-1992; 92FR-0007571.  
 XX 22-JUN-1992; 92FR-0007571.  
 XX (PEREZ/) PEREZ J.  
 XX Perez J;  
 XX WPI; 1994-028256/04.  
 XX N-PSDB; AA055629, AA055630.  
 XX Application of optimised gene expression - for scientific,  
 XX industrial and therapeutic purposes  
 XX Disclosure: Fig 28 and Fig 29; 110pp; French.  
 XX Resonances between coding and non-coding regions were measured for  
 CC the native human IL-2 gene in plasmid pT911 (see AA055630) and a  
 CC synthetic IL-2 gene (AA055629) in which alternative, degenerate  
 CC codons were used in order to introduce additional restriction  
 CC sites. It was found that the degenerate changes greatly upset the  
 CC "natural order" between coding and non-coding regions; as a result,  
 CC the amount of protein expressed by the degenerate gene is likely to  
 CC be adversely affected. The inventors have proposed an "optimised"  
 CC IL-2 gene with the aim of increasing the amount of protein expressed  
 CC by the gene. (N.B. the sequence is also described as  
 CC interleukin-6).  
 CC XX  
 SQ Sequence 60 AA;  
 Query Match 100.0%; Score 152; DB 15; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 4, 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQQLQLEHLIDLMQILNGINN 31  
 DB 1 MAPTSSSTKKTQQLQLEHLIDLMQILNGINN 31  
 RESULT 5  
 AAR68899  
 ID AAR68899 standard; peptide; 96 AA.  
 XX AAR68899;  
 XX 02-MAR-1995 (first entry)  
 XX Human pro-insulin 2.  
 XX DE Human pro-insulin 2.  
 XX KW Pro-insulin; A-chain; B-chain; C-chain; disulphide;  
 XX mercaptan; chaotropic agent.  
 XX XX  
 OS Homo sapiens.  
 XX EP600372-A.  
 XX PN 08-JUN-1994.  
 XX PD 25-NOV-1993; 93EP-0118993.  
 XX PF 02-DEC-1992; 92DE-4240420.  
 XX PR (FARH ) HOECHST AG.  
 XX PA  
 XX XX

PI Gerl M, Ludwig J, Obermeier R, Sabel W;  
 XX WPI; 1994-177718/22.  
 XX prodn. of pro-insulin with correct di:sulphide bridges - by  
 XX treating recombinant precursor protein with mercaptan in alkali  
 XX and in presence of chaotropic agent, then isolation on  
 XX hydrophobic resin  
 XX XX  
 PS Disclosure; Page 11; 15pp; German.  
 XX CC Pro-insulin is produced by treating recombinant precursor protein  
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in  
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,  
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.  
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and  
 CC desorbing the pro-insulin. This method produces pro-insulin with  
 CC correctly bonded Cys bridges. Compared with known methods it  
 CC involves fewer stages (esp. no sulphitolysis or cyanogen bromide  
 CC cleavage) and overall losses during purification are reduced, i.e.  
 CC the process is quicker and gives better yields.  
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.  
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.  
 CC XX  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 152; DB 15; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQQLQLEHLIDLMQILNGINN 31  
 DB 1 MAPTSSSTKKTQQLQLEHLIDLMQILNGINN 31  
 RESULT 6  
 AAR78662  
 ID AAR78662 standard; protein; 96 AA.  
 XX AAR78662;  
 XX 03-APR-1996 (first entry)  
 XX Fusion protein contg. proinsulin sequence 3.  
 XX DE Proinsulin; post-translational modification; recombinant production;  
 XX KW protein folding; conformation.  
 XX XX  
 OS Synthetic.  
 XX OS  
 XX Key Location/Qualifiers  
 XX FH 41..44  
 XX FT Region /label= R2  
 XX FT /note= "a peptide of 4 amino acids"  
 XX FT 45..74  
 XX FT Peptide /label= RL-(B2-B29)-Y  
 XX FT /note= "human Insulin B-chain"  
 XX FT Region 75  
 XX FT /label= X  
 XX FT Peptide 76..96  
 XX FT /label= Gly-(A2-A20)-R3  
 XX FT /note= "human Insulin A-chain"  
 XX XX  
 XX EP668292-A2.  
 XX PN 23-AUG-1995.  
 XX PD 09-FEB-1995; 95EP-0101748.  
 XX PF 18-FEB-1994; 94DE-4405179.  
 XX PR (FARH ) HOECHST AG.  
 XX PA  
 XX XX

PI Gerl M, Ludwig J, Obermeier R, Sabel W:  
 DR MPI: 1995-284754/38.  
 PT Isolation of insulin that is correctly post-translationally  
 processed - by reacting pro-insulin with a mercaptan in the presence  
 of a chaotropic agent and purification after absorption to hydrophobic  
 resin  
 XX  
 PS Example 2: Page 8: 16pp: German.  
 CC The present sequence is that of a fusion protein, produced in E. coli  
 CC which contains an example of a proinsulin molecule corresp.  
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In  
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.  
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =  
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids  
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino  
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences  
 CC from human or other insulin. The proinsulin molecule, released by  
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH  
 CC residues of mercaptan per Cys residue of proinsulin. The reaction  
 CC takes place in the presence of a chaotropic auxiliary agent at  
 CC pH 10-11 and results in proinsulin and correctly linked cystine  
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields  
 CC correctly folded insulin. The insulin is isolated by absorption on  
 CC a hydrophobic resin.  
 SO Sequence 96 AA:  
 Query Match 100.0%; Score 152; DB 16; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPTSSSTKKTQLQLEHLLDLQMLINGINN 31  
 DB 1 MAPTSSSTKKTQLQLEHLLDLQMLINGINN 31  
 RESULT 7  
 AAR22595  
 ID AAR22595 standard; Protein: 133 AA.  
 AC AAR22595;  
 DT 03-NOV-1992 (first entry)  
 DE Interleukin-2 used to make hybrid proteins.  
 XX IL-2: hybrid; diphtheria; toxin; DT; proliferation; peripheral blood;  
 KM mononuclear cells; PHMC; auto-immune response; diabetes; rheumatoid;  
 KM arthritis; allograft rejection; T-suppressor.  
 OS Homo sapiens.  
 XX WO9206117-A.  
 PN 16-APR-1992.  
 PD 27-SEP-1991; 91MO-US07342.  
 PF 28-SEP-1990; 90US-0590113.  
 PR (SERRA-) SERAGEN INC.  
 PA (UTHO-) UNIVERSITY HOSPITAL.  
 XX Murphy JR, Svrluga R;  
 PI MPI: 1992-150820/18.  
 DR N-PSDB; AAQ23867.  
 XX  
 PT Hybrid protein comprising portion of the IL-2 binding domain -  
 useful for inhibiting unwanted immune responses e.g. autoimmune

PT diseases and reaction to organ and tissue transplants  
 XX Disclosure; Fig 1: 37pp; English.  
 PS  
 CC The interleukin-2 protein is part of a hybrid protein comprising  
 CC the binding domain of IL-2 and an enzymatically inactive fragment  
 CC of diphtheria toxin which does not include a functional DT  
 CC generalised eukaryotic binding site (see AAR26485). The hybrid  
 CC protein is capable of stimulating the proliferation of peripheral  
 CC blood mononuclear cells in vitro and of suppressing an immune  
 CC response in a mammal in vivo. The hybrid protein allows the  
 CC inhibition of an unwanted immune response such as autoimmune disease,  
 CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It  
 CC does not cause general immunosuppression, so avoids the resulting  
 CC risk of life threatening infections. In the treatment of allograft  
 CC rejection the hybrid protein spares donor-specific T-suppressor cells,  
 CC which can thus proliferate and aid in prolonging graft survival. The  
 CC hybrid protein does not need to be tailored to individual patients but  
 CC can be used as a universal inhibiting agent. Therapy need not be  
 CC continuous following allograft or an acute stage of autoimmune  
 CC disease, but can be discontinued after a course of treatment.  
 SO Sequence 133 AA:  
 Query Match 100.0%; Score 152; DB 13; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPTSSSTKKTQLQLEHLLDLQMLINGINN 31  
 DB 1 MAPTSSSTKKTQLQLEHLLDLQMLINGINN 31  
 RESULT 8  
 AAP40050  
 ID AAP40050 standard; Protein: 134 AA.  
 AC AAP40050;  
 DT 14-JAN-1992 (first entry)  
 DE Sequence of an interleukin-2-like polypeptide encoded by the DNA  
 DE insert of pSV-hIL2-O or pSV-hIL2-1.  
 XX  
 KM Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;  
 KM multiple sclerosis; lupus; rheumatoid arthritis; herpes;  
 KM viral disease; lymphokine.  
 OS Homo sapiens.  
 XX EPL18977-A.  
 PN 19-SEP-1984.  
 PD 25-JAN-1984; 84EP-0300439.  
 PF 10-JUN-1983; 83GB-0015981.  
 PR 08-FEB-1983; 83GB-0003383.  
 XX (BIOJ ) BIOGEN NV.  
 PA  
 PI Fiers WC, Devos RR;  
 DR MPI: 1984-232548/38.  
 DR N-PSDB; AAN40042.  
 XX  
 PT Prodn. of human interleukin-2-like polypeptide(s) - useful  
 PT instead of IL-2 for stimulating the immune system etc.  
 XX  
 PS Claim 6: Page 57-58; 69pp; English.  
 CC The DNA sequence is esp. selected from a human chromosomal gene bank,  
 CC e.g. it is a hIL-2 related portion of lambda CH4A-ghIL-2-1 or -2, or

CC of Iamda L47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,  
CC esp. E.coli, Ps spp., B.subtilis, B.stearothermophilus. IL-2-like  
CC polypeptides are also claimed.

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31  
DB 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31

RESULT 9

AAP50053 standard; Protein: 134 AA.

AC AAP50053:

DT 03-SEP-1991 (first entry)

XX Sequence 1 of new biologically active interleukin 2 (IL-2).

XX Immunological agent; lymphokine.

XX EPI63249-A.

PD 04-DEC-1985.

XX 28-MAY-1985; 85EP-0113324.

PR 29-MAY-1984; 84DE-3419995.

PA (FARH) HOECHST AG.

PI Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;

PI Wertz R, Okazaki H;

DR WPI: 1985-304738/49.

DR N-PSDB; AAN50037.

XX New biologically active interleukin 2 fragments and derivs. - and  
XX coding DNA sequences, intermediate oligo-nucleotide(s), hybrid  
XX plasmid(s) and transformed cells

PS Disclosure: Page 18-20; 33pp; German.

CC DNA SCS coding for AAs 1-133 and 0-133 (an additional Met) of IL-2  
CC are claimed, including the CDS of SQ 1 (see AAN50037) with/without  
CC or 2 stop codons. The use of a synthetic gene is esp. convenient  
CC for expression in E. coli and allows modification of the AA SO to  
CC improve peptide stability, solubility or activity. The synthetic  
CC gene was made from a series of oligonucleotides ligated to form four  
CC larger fragments designated IL 2-I to 2-IV (see AAN50038).

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31  
DB 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31

RESULT 10

AAP50855 standard; Protein: 134 AA.

XX AAP50855:

XX 01-DEC-1991 (first entry)

XX Sequence encoded by synthetic interleukin II (IL-2) gene.

XX Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

XX WO8500817-A.

XX 28-FEB-1985.

XX 09-AUG-1984; 84WO-US01252.

XX 03-AUG-1984; 84US-0635941.

XX 10-AUG-1983; 83US-0521967.

XX (AMGE-) AMGEN.

XX Souza LM, Stabinsky Y;

XX WPI: 1985-062280/10.

XX N-PSDB; AAN50535.

XX Microbial expression of interleukin II and analogues - by using  
XX PT manufactured DNA sequences to transform microorganisms

XX Example; Table IV, Page 15-16; 39pp; English.

CC The inventors claim a manufactured gene for the prodn. of IL-2 and  
CC analogues, and for polypeptides of IL-2 and analogues, and for  
CC methods for their recombinant production.

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31  
DB 1 MAPTSSSTKKTQLEHLLDLOMILNGINN 31

RESULT 11

AAP61102 standard; Protein: 134 AA.

AC AAP61102:

DT 09-MAR-1992 (first entry)

XX Sequence of mature human interleukin 2 (IL2) encoded by SUN-112.

XX Yeast expression vector; lymphokine.

XX Homo sapiens.

XX EPI71000-A.

XX 12-FEB-1986.

XX 26-JUL-1985; 85EP-0109405.

XX 27-JUL-1984; 84JP-0157038.

XX (SUNR) SUNTORY LTD.

XX Oshima T, Tanaka S, Tsujimoto M, Nakazato H;

XX WPI: 1986-043554/07.

XX N-PSDB; AAN60198.

XX Protein and peptide prodn. by immobilised yeast transformant -

PT contg. expression vector which induces secretion of prod. from  
 XX cell into culture medium  
 PS Disclosure: Fig 6 and Page 31; 53pp; English.  
 CC The inventors claim a method for the prodn. of a substance having  
 CC the AA SQ of AAF61102. The method uses a synthetic DNA SQ (AAN60198). A  
 CC composition contg. a protein having human IL2 activity which is  
 CC produced by the method is also claimed. The method uses yeast  
 CC transformed by a secretory expression vector.  
 XX  
 SO Sequence 134 AA;  
 Query Match 100.0%; Score 152; DB 7; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQLOLEHLLDLOMILNGINN 31  
 DB 1 MAPTSSSTKKTQLOLEHLLDLOMILNGINN 31  
 RESULT 12  
 ID AAF70585 standard; protein: 134 AA.  
 XX AAF70585;  
 AC AAF70585;  
 XX 10-APR-1991 (first entry)  
 DT  
 XX Sequence of human Interleukin-2 (IL-2).  
 DE  
 XX Lymphokine.  
 KW  
 XX Homo sapiens.  
 OS  
 XX DE3541856-A.  
 PN  
 XX 04-JUN-1987.  
 PD  
 XX 27-NOV-1985; 85DE-3541856.  
 PF  
 XX 27-NOV-1985; 85DE-3541856.  
 PR  
 XX (FARH ) HOECHST AG.  
 PA  
 XX Habermann P, Wengenmayer F;  
 PI  
 XX WPI; 1987-157830/23.  
 DR  
 XX N-PSDB; AAN70931.  
 DT  
 XX Fusion proteins contg. interleukin 2 aminoacid sequences - as  
 PT well as genes coding for these proteins, vectors contg. the  
 PT genes, and host cells contg. the vectors  
 PS Example: pp 7-8, 20pp; German.  
 XX  
 CC Prefd. fusion proteins are of formula Met-X-Y-Z or Met-Z-Y-X. Where  
 CC X=an AA sequence corresp. essentially to approx. the first 100 AAs  
 CC of human interleukin-2; Y=a direct bond or bridge of genetically  
 CC codable AAs which facilitates the cleaving off of the AA sequence Z;  
 CC Z=a sequence of genetically codable AAs.  
 XX  
 SO Sequence 134 AA;  
 Query Match 100.0%; Score 152; DB 8; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPTSSSTKKTQLOLEHLLDLOMILNGINN 31  
 DB 1 MAPTSSSTKKTQLOLEHLLDLOMILNGINN 31

RESULT 13  
 ID AAR05267 standard; protein: 134 AA.  
 XX AAR05267;  
 AC AAR05267;  
 XX  
 DT 04-AUG-1990 (first entry)  
 DT  
 XX Sequence of naturally occurring human Interleukin-2 (IL-2).  
 DE  
 XX Interleukin-2 (IL-2); biological assays.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 XX FH 12..19  
 XX FT /note="helix A"  
 XX FT 33..46  
 XX FT /note="helix B"  
 XX FT 48..56  
 XX FT /note="helix B"  
 XX FT 66..78  
 XX FT /note="helix C"  
 XX FT 83..101  
 XX FT /note="helix D"  
 XX FT 106..113  
 XX FT /note="helix E"  
 XX FT 117..13  
 XX FT /note="helix F"  
 XX PN  
 XX WO9000565-A.  
 XX PD 25-JAN-1990.  
 XX PF 05-JUL-1989; 89WO-US02917.  
 XX PR 05-JUL-1989; 88US-0214998.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI  
 XX PI Alttrock B, Boone TC, Goldman RA, Kenny WC, Strabinsky Y;  
 DR WPI; 1990-051690/07.  
 DR N-PSDB; AAO04812.  
 DT  
 XX Improved interleukin-II analogues -  
 PT eg with ability to attach toxins, reporter gns. or therapeutic  
 PT cpds.  
 PS Table 1; Page 25; 52pp; English.  
 XX  
 CC Site directed mutagenesis procedures were carried out on the DNA  
 CC sequence encoding this to generate analogues of IL-2 using the  
 CC oligonucleotides in AAN92950-n92959. Claim 1 claims it wherein at least  
 CC one of AAs 47, 51, 80, 81, 106, 109, 112, 119, 120, 123, 127, 129,  
 CC 131, and 133 in the original amino acid sequence is replaced by a  
 CC substitution, amino acid residue, or wherein at least two of the 8th,  
 CC 47th, 48th, 51st, 54th, 80th, 81st, 106th, 109th, 112th, 119th,  
 CC 120th, 121st, 123rd, 127th, 129th, 130th, 131st, 132nd and  
 CC 133rd original amino acid residues are replaced by substitution  
 CC amino acid residues. The following 10 analogues of IL-2 are  
 CC specifically claimed: (Cys 8)-, (Gly 47)-, (Asp 51)-, (Cys 80)-,  
 CC (Cys 81)-, (Lys 106)-, (Lys 112)-, (Cys 132)-, (Cys 134)- IL-2.  
 CC Analogues have been constructed to which other molecules can be  
 CC covalently attached without damaging activity. These analogues are used  
 CC to attack toxins, reporter gns. or antiviral or other therapeutic cpds.,  
 CC providing IL-2 conjugates for therapy, or specifically labelled IL-2 for  
 CC development of sensitive biological assays.  
 XX  
 SO Sequence 134 AA;  
 Query Match 100.0%; Score 152; DB 11; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQOLEHLLDLOMIINGINN 31  
DB 1 MAPTSSSTKKTQOLEHLLDLOMIINGINN 31

RESULT 14  
AAR05266  
ID AAR05266 standard; protein; 134 AA.  
AC AAR05266;  
XX  
XX 04-AUG-1990 (first entry)  
DT  
XX  
XX Sequence of naturally occurring human Interleukin-2 (IL-2).  
DE  
XX  
XX Interleukin-2 (IL-2); biological assays.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Region 12..19  
FT /note="helix A"  
FT 33..46  
FT /note="helix B"  
FT 48..56  
FT /note="helix B'"  
FT 66..78  
FT /note="helix C"  
FT 83..101  
FT /note="helix D"  
FT 106..113  
FT /note="helix E"  
FT 117..13  
FT /note="helix F"  
XX  
XX  
XX WO9000565-A.  
PN  
XX  
XX 25-JAN-1990.  
PD  
XX  
XX 05-JUL-1989; 89WO-US02917.  
PF  
XX  
XX 05-JUL-1988; 88US-0214998.  
PR  
XX  
XX (AMGE-) AMGEN INC.  
PA  
XX  
XX Altrock B, Boone TC, Goldman RA, Kenny WC, Stabinsky Y;  
PI  
XX  
XX WPI; 1990-051690/07.  
DR  
XX  
XX N-PSDB; AA004811.  
XX  
XX  
XX Improved interleukin-II analogues -  
PT eg with ability to attach toxins, reporter gps. or therapeutic  
PT cpds.  
XX  
XX  
XX Disclosure; Table 1, Page 25; 52pp; English.  
XX  
XX Site directed mutagenesis procedures were carried out on the DNA  
CC sequence encoding this to generate analogues of IL-2 using the  
CC oligonucleotides in AAN92950-092959. Claim 1 claims it wherein at least  
one of AAs 47, 51, 80, 81, 106, 109, 112, 119, 120, 123, 127, 129,  
131, and 133 in the original amino acid sequence is replaced by a  
CC substitution amino acid residue, or wherein at least two of the 8th,  
CC 47th, 48th, 51st, 54th, 80th, 81st, 106th, 109th, 112th, 119th,  
CC 120th, 121st, 123rd, 127th, 129th, 130th, 131st, 132nd and  
CC 133rd original amino acid residues are replaced by substitution  
CC amino acid residues. The following 10 analogues of IL-2 are  
CC specifically claimed: (Cys 8)-, (Gly 47)-, (Asp 51)-, (Cys 80)-,  
CC (Cys 81)-, (Lys 106)-, (Lys 112)-, (Cys 132)-, (Cys 134)- IL-2.  
CC Analogues have been constructed to which other molecules can be  
CC covalently attached without damaging activity. These analogues are used

CC to attack toxins, reporter gps. or antiviral or other therapeutic cpds.,  
CC providing IL-2 conjugates for therapy, or specifically labelled IL-2 for  
CC development of sensitive biological assays.

XX  
XX  
XX Sequence 134 AA;  
SQ

Query Match 100.0%; Score 152; DB 11; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQOLEHLLDLOMIINGINN 31  
DB 1 MAPTSSSTKKTQOLEHLLDLOMIINGINN 31

RESULT 15  
AAR05240  
ID AAR05240 standard; protein; 134 AA.  
AC AAR05240;  
XX  
XX  
XX 04-AUG-1990 (first entry)  
DT  
XX  
XX Sequence of naturally occurring human Interleukin-2 (IL-2).  
DE  
XX  
XX Interleukin-2 (IL-2); biological assays.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Region 12..19  
FT /note="helix A"  
FT 33..46  
FT /note="helix B"  
FT 48..56  
FT /note="helix B'"  
FT 66..78  
FT /note="helix C"  
FT 83..101  
FT /note="helix D"  
FT 106..113  
FT /note="helix E"  
FT 117..13  
FT /note="helix F"  
XX  
XX  
XX WO9000565-A.  
PN  
XX  
XX 25-JAN-1990.  
PD  
XX  
XX 05-JUL-1989; 89WO-US02917.  
PF  
XX  
XX 05-JUL-1988; 88US-0214998.  
PR  
XX  
XX (AMGE-) AMGEN INC.  
PA  
XX  
XX Altrock B, Boone TC, Goldman RA, Kenny WC, Stabinsky Y;  
PI  
XX  
XX WPI; 1990-051690/07.  
DR  
XX  
XX N-PSDB; AA003325.  
XX  
XX  
XX Improved interleukin-II analogues -  
PT eg with ability to attach toxins, reporter gps. or therapeutic  
PT cpds.  
XX  
XX  
XX Disclosure; page 25; 52pp; English.  
XX  
XX Site directed mutagenesis procedures were carried out on DNA sequence  
CC encoding this to generate analogues of IL-2 using the oligonucleotides  
CC in AAN92950-092959. Claim 1 claims it wherein at least one of AAs 47,  
CC 51, 80, 81, 106, 109, 112, 119, 120, 123, 127, 129,  
CC 131, and 133 of the original amino acid sequence is replaced by a  
CC substitution amino acid residue, or wherein at least two of the 8th,  
CC 47th, 48th, 51st, 54th, 80th, 81st, 106th, 109th, 112th, 119th,

CC 120th, 121st, 123rd, 127th, 129th, 130th, 131st, 132nd and  
 CC 133rd original amino acid residues are replaced by substitution  
 CC amino acid residues. The following 10 analogues of IL-2 are  
 CC specifically claimed: (Cys 8)-, (Gly 47)- (Asp 51)-, (Cys 80)-,  
 CC (Cys 81)-, (Lys 105)-, (Lys 112)-, (Cys 132)-, (Cys 134)- IL-2.  
 CC Analogues have been constructed to which other molecules can be  
 CC covalently attached without damaging activity. These analogues are used  
 CC to attack toxins, reporter gps. or antiviral or other therapeutic cpds.,  
 CC providing IL-2 conjugates for therapy, or specifically labelled IL-2 for  
 CC development of sensitive biological assays.  
 XX

XX Sequence 134 AA;

Query Match 100.0%; Score 152; DB 11; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.2e-13; Mismatches 0; Gaps 0;

Matches 31; Conservative 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLDQMTINGINN 31  
 DB 1 MAPTSSSTKKTQLEHLLDQMTINGINN 31

Search completed: October 25, 2002, 15:48:33  
 Job time : 32 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:46:51 : Search time 13 Seconds  
(Without alignments)  
58.246 Million cell updates/sec

Title: US-09-720-828A-2

Sequence: 152  
1 MAPSSSTKKTQLEHLLDQMLINGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	100.0	31	4 US-09-116-594-2	Sequence 2, Appli
2	152	100.0	96	1 US-08-160-376A-5	Sequence 5, Appli
3	152	100.0	96	1 US-08-389-487-8	Sequence 8, Appli
4	152	100.0	134	6 5496924-55	Patent No. 5496924
5	147	96.7	50	1 US-08-127-351-13	Sequence 13, Appli
6	147	96.7	50	1 US-08-480-367B-13	Sequence 13, Appli
7	147	96.7	50	1 US-08-487-221A-13	Sequence 13, Appli
8	147	96.7	50	1 US-08-480-370-13	Sequence 13, Appli
9	147	96.7	88	4 US-08-817-787-15	Sequence 15, Appli
10	147	96.7	133	1 US-08-817-787-15	Sequence 15, Appli
11	147	96.7	133	1 US-07-800-366-1	Sequence 5, Appli
12	147	96.7	133	1 US-08-354-456A-5	Sequence 5, Appli
13	147	96.7	133	1 US-08-225-224-3	Sequence 89, Appli
14	147	96.7	133	1 US-08-318-193-89	Sequence 1, Appli
15	147	96.7	133	1 US-08-284-393B-2	Sequence 2, Appli
16	147	96.7	133	1 US-08-284-393B-2	Sequence 3, Appli
17	147	96.7	133	1 US-08-284-393B-2	Sequence 3, Appli
18	147	96.7	133	1 US-08-734-471-1	Sequence 1, Appli
19	147	96.7	133	1 US-08-734-471-1	Sequence 1, Appli
20	147	96.7	133	4 US-08-817-787-13	Sequence 13, Appli
21	147	96.7	133	4 US-09-310-026-1	Sequence 1, Appli
22	147	96.7	133	5 PCT-US95-04468-3	Sequence 3, Appli
23	147	96.7	133	5 PCT-US95-08950-1	Sequence 1, Appli
24	147	96.7	133	5 PCT-US95-08950-2	Sequence 2, Appli
25	147	96.7	133	5 PCT-US95-08950-3	Sequence 3, Appli
26	147	96.7	133	6 5210029-1	Patent No. 5210029
27	147	96.7	133	6 5256769-1	Patent No. 5256769
	147	96.7	133	6 5464939-2	Patent No. 5464939

28	147	96.7	153	3 US-09-012-366-3	Sequence 3, Appli
29	147	96.7	153	4 US-08-759-628-8	Sequence 8, Appli
30	147	96.7	153	4 US-09-522-217-111	Sequence 111, App
31	147	96.7	153	6 5314995-7	Patent No. 5314995
32	147	96.7	157	4 US-08-818-562-2	Sequence 2, Appli
33	147	96.7	478	3 US-08-155-888-2	Sequence 2, Appli
34	147	96.7	504	1 US-07-932-915-2	Sequence 2, Appli
35	147	96.7	504	5 PCT-US91-05826-2	Sequence 2, Appli
36	144	94.7	251	3 US-08-875-811-59	Sequence 59, Appli
37	144	94.7	254	3 US-08-875-811-61	Sequence 61, Appli
38	143	94.1	133	1 US-08-354-456A-6	Sequence 6, Appli
39	132.5	87.2	127	3 US-08-806-121B-3	Sequence 3, Appli
40	107	70.4	141	4 US-08-930-917A-18	Sequence 18, Appli
41	79	52.0	135	2 US-08-383-621-5	Sequence 5, Appli
42	79	52.0	135	3 US-08-459-906-5	Sequence 5, Appli
43	79	52.0	1098	1 US-07-777-715-7	Sequence 7, Appli
44	79	52.0	1098	1 US-08-170-126-2	Sequence 2, Appli
45	79	52.0	1098	3 US-08-954-418-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-116-594-2
: Sequence 2, Application US/09116594
: Patent No. 6168785
: GENERAL INFORMATION:
: APPLICANT: THEZE, Jacques
: APPLICANT: ECKENBERG, Ralph
: APPLICANT: MOREAU, Jean-Louis
: APPLICANT: MAZIE, Jean-Claude
: TITLE OF INVENTION: BIOLOGICAL APPLICATIONS OF NEW PEPTIDES OF IL-2 AND
: TITLE OF INVENTION: DERIVATIVES AND USE AS THERAPEUTIC AGENTS
: FILE REFERENCE: 0660-0134-0
: CURRENT FILING DATE: 1998-07-16
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 2
: LENGTH: 31
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-116-594-2
Query Match 100.0%; Score 152; DB 4; Length 31;
Best Local Similarity 100.0%; Pred.No. 3.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C/ 1 MAPSSSTKKTQLEHLLDQMLINGINN 31
Db 1 MAPSSSTKKTQLEHLLDQMLINGINN 31
RESULT 2
US-08-160-376A-5
: Sequence 5, Application US/08160376A
: Patent No. 5473049
: GENERAL INFORMATION:
: APPLICANT: Obermeier, Rainer
: APPLICANT: Gerl, Martin
: APPLICANT: Ludwig, Jurgen
: APPLICANT: Sabel, Walter
: TITLE OF INVENTION: Process For Obtaining Proinsulin
: TITLE OF INVENTION: Possessing Correctly Linked
: TITLE OF INVENTION: Cystine Bridges
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth A. Genoni, Esq.
: STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
: CITY: Somerville
```

STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 08876-1258  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 386  
OPERATING SYSTEM: WINDOWS 3.1  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/160,376A  
FILING DATE: December 1, 1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GE P 4240420.7  
FILING DATE: December 2, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barbara V. Maurer, Esq.  
REGISTRATION NUMBER: 31,287  
REFERENCE/DOCKET NUMBER: HOE 92/F 384  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 231-4079  
TELEFAX: (908) 231-2255  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 Amino Acids  
TYPE: Amino Acid (AA)  
TOPOLOGY: not relevant  
US-08-160-376A-5

Query Match 100.0%; Score 152; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31  
DB 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31

RESULT 3  
US-08-389-487-8  
Sequence 8, Application US/08389487  
Patent No. 5663291  
GENERAL INFORMATION:  
APPLICANT: Obermeyer, Rainer  
APPLICANT: Geil, Martin  
APPLICANT: Ludwig, Jurgen  
APPLICANT: Sabel, Walter  
TITLE OF INVENTION: Process for Obtaining Insulin Having  
TITLE OF INVENTION: Correctly Linked Cysteine Bridges  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &  
ADDRESS: Dunnet  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/389,487  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Finnudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02401.1424-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-389-487-8

Query Match 100.0%; Score 152; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31  
DB 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31

RESULT 4  
5496924-55  
Patent No. 5496924  
APPLICANT: HABERMANN, PAUL; WENGENMAYER, FRIEDRICH  
TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN  
INTERLEUKIN-2 FRAGMENT BALLAST PORTION  
NUMBER OF SEQUENCES: 56  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,545  
FILING DATE: 28-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 377,313  
FILING DATE: 10-JUL-1989  
APPLICATION NUMBER: 934,910  
FILING DATE: 25-NOV-1986  
APPLICATION NUMBER: 943,804  
FILING DATE: 19-DEC-1986  
SEQ ID NO: 55  
LENGTH: 134  
5496924-55

Query Match 100.0%; Score 152; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31  
DB 1 MAPSSSTKKTQLQLEHLLDLOMTLNGINN 31

RESULT 5  
US-08-127-351-13  
Sequence 13, Application US/08127351  
Patent No. 5449761  
GENERAL INFORMATION:  
APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCUELLAND, MAIER &  
ADDRESS: NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,351  
FILING DATE: 28-SEP-1993  
CLASSIFICATION: 534  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855\OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-127-351-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 APTSSSTKKTQLEHLLDLMQILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMQILNGINN 30

RESULT 6  
US-08-480-367B-13  
Sequence 13, Application US/08480367B  
Patent No. 5578288  
GENERAL INFORMATION:  
APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,367B  
FILING DATE: 07-06-95  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 2654-002A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 684-1111  
TELEFAX: (703) 684-1124  
TELEX: (703) 684-1124  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-480-367B-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 APTSSSTKKTQLEHLLDLMQILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMQILNGINN 30

RESULT 7  
US-08-487-221A-13  
Sequence 13, Application US/08487221A  
Patent No. 5593656  
GENERAL INFORMATION:  
APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
ADDRESSEE: NEUSTADY, P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,221A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-487-221A-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 APTSSSTKKTQLEHLLDLMQILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMQILNGINN 30

RESULT 8  
US-08-480-370-13  
Sequence 13, Application US/08480370  
Patent No. 5609847  
GENERAL INFORMATION:

APPLICANT: BELINKA, J.T., BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MATER &  
ADDRESSEE: NEWSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,370  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-480-370-13  
Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 APTSSSTKKTQQLQLEHLLDLMQMLNGINN 31  
DB 1 APTSSSTKKTQQLQLEHLLDLMQMLNGINN 30  
RESULT 9  
US-08-817-787-15  
Sequence 15, Application US/08817787  
Patent No. 6294353  
GENERAL INFORMATION:  
APPLICANT: Pack, Peter  
APPLICANT: Lupas, Andrei  
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF  
RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,787  
FILING DATE: 23-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04117  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94 11 6558.1  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 88 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-817-787-15  
Query Match 96.7%; Score 147; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 7.2e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 APTSSSTKKTQQLQLEHLLDLMQMLNGINN 31  
DB 3 APTSSSTKKTQQLQLEHLLDLMQMLNGINN 32  
RESULT 10  
US-07-800-366-1  
Sequence 1, Application US/07800366  
Patent No. 5250296  
GENERAL INFORMATION:  
APPLICANT: OOTSU, Koichiro  
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING  
INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/800,366  
FILING DATE: 19911127  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Castle, Donald R.  
REGISTRATION NUMBER: 24,220  
REFERENCE/DOCKET NUMBER: 41417(281)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-800-366-1

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLLDQMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLLDQMILNGINN 30

RESULT 11  
US-08-354-456A-5  
Sequence 5, Application US/08354456A  
Patent No. 5567611

GENERAL INFORMATION:  
APPLICANT: Ralph, Peter  
APPLICANT: Martin, George  
APPLICANT: Patrick, Michael  
APPLICANT: Larrick, James W.  
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding  
TITLE OF INVENTION: Therefore  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: CHIRON CORPORATION  
STREET: Intellectual Property - R440, P.O. Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,456A  
FILING DATE: 12-DEC-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/995,338  
FILING DATE: 21-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: McGarrigle Jr., Philip L.  
REGISTRATION NUMBER: 31,395  
REFERENCE/DOCKET NUMBER: 750,003/32387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2718  
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-456A-5

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLLDQMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLLDQMILNGINN 30

RESULT 12

US-08-225-224-3  
Sequence 3, Application US/08225224  
Patent No. 5635599

GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
APPLICANT: KREITMAN, Robert J.  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..133  
OTHER INFORMATION: /label= IL2

US-08-225-224-3

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLLDQMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLLDQMILNGINN 30

RESULT 13  
US-08-318-193-89  
Sequence 89, Application US/08318193  
Patent No. 5641663

GENERAL INFORMATION:  
APPLICANT: GARVIN, Robert T.  
APPLICANT: MAHER, Lawrence T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION  
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY  
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 1800 diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299

US-08-318-193-89

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)836-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-193-89

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLHLLDQMLINGINN 31  
DB 1 APTSSSTKKTQLEHLHLLDQMLINGINN 30

RESULT 14  
US-08-284-393B-1  
Sequence 1, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MYEINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-1

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLHLLDQMLINGINN 31  
DB 1 APTSSSTKKTQLEHLHLLDQMLINGINN 30

RESULT 15  
US-08-284-393B-2  
Sequence 2, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MYEINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-2

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLHLLDQMLINGINN 31  
DB 1 APTSSSTKKTQLEHLHLLDQMLINGINN 30

Search completed: October 25, 2002, 15:49:43  
Job time : 15 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:48:06 ; Search time 15 Seconds  
(without alignments)  
198.585 Million cell updates/sec

Title: US-09-720-828A-2

Sequence: 1 MAFPSSTKRTOLQLEHLDDMLNGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Print. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	147	96.7	153	1 ICH02	interleukin-2 prec
2	147	96.7	153	1 ICG12	interleukin-2 prec
3	114	75.0	154	2 JMO658	interleukin 2 prec
4	97	63.8	155	2 A31278	interleukin-2 prec
5	96	63.2	154	2 S16241	interleukin-2 prec
6	95	62.5	155	2 S33509	interleukin-2 - Mo
7	92	60.5	149	2 S31391	interleukin-2 prec
8	79	52.0	155	2 S38662	interleukin-2 - go
9	79	52.0	155	2 S11488	interleukin-2 prec
10	79	52.0	155	2 I45913	interleukin-2 prec
11	69	45.4	169	2 S37289	interleukin-2 prec
12	64	42.1	169	1 ICM52	interleukin-2 prec
13	59.5	39.1	60	2 I68870	interleukin-2 - we
14	58.5	38.5	62	2 I54512	interleukin 2 - mo
15	57.5	37.8	72	2 I68871	interleukin 2 - mo
16	54	35.5	357	2 S12169	isopenicillin N ac
17	52	34.2	155	1 F64145	hypothetical prote
18	52	34.2	737	2 G82262	probable exopolysa
19	51	33.6	304	2 P95285	probable lysR type
20	51	33.6	627	2 E70122	flagellar hook-ass
21	50	32.9	365	2 C70701	hypothetical prote
22	49	32.2	230	2 H82447	DNA-binding respon
23	49	32.2	543	2 F82217	methyl-accepting c
24	49	32.2	1130	2 A89130	protein F52B1.4 [l
25	48.5	31.9	240	2 T22210	hypothetical prote
26	48	31.6	189	2 H64307	hypothetical prote
27	48	31.6	441	2 AB1367	aminopeptidase C l
28	48	31.6	441	2 AC1736	aminopeptidase C l
29	48	31.6	1061	1 GMLJG4	pol polyprotein -

30	47.5	31.2	244	2 T11685	hypothetical prote
31	47.5	31.2	2	F86548	polymorphic outer
32	47.5	31.2	2	H72074	polymorphic membra
33	47	30.9	398	2 B70209	conserved hypotet
34	47	30.9	2	F89839	hypothetical prote
35	47	30.9	1008	2 T41244	SEC14 protein homo
36	46.5	30.6	159	2 T05656	nonmuscle myosin I
37	46.5	30.6	211	2 C84888	hypothetical prote
38	46.5	30.6	2	E90228	hypothetical prote
39	46.5	30.6	466	2 A71946	amino acid specifi
40	46	30.3	293	2 H90434	hypothetical prote
41	46	30.3	323	2 C37760	hypothetical prote
42	46	30.3	380	1 B64551	galactokinase (EC
43	46	30.3	516	2 B64551	oligopeptide ABC t
44	46	30.3	571	2 H82355	peptide ABC transp
45	46	30.3	614	2 T18745	hypothetical prote

ALIGNMENTS

RESULT 1

Interleukin-2 precursor [validated] - human

N:Alternate names: IL-2; T-cell growth factor

C:Species: Homo sapiens (man)

C:Date: 11-Aug-1983 #sequence, revision 11-Aug-1983 #text, change 08-Dec-2000

C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;

R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.

A>Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo

A:Reference number: A93524; MUID:84247353

A:Accession: A01849

A:Molecule type: DNA

A:Residues: 1-153 <HOL>

A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2

R:Fujita, T.; Takeoka, C.; Matsui, H.; Taniguchi, T.

Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983

A>Title: Structure of the human interleukin 2 gene.

A:Reference number: A21192; MUID:84170243

A:Accession: A21192

A:Molecule type: DNA

A:Residues: 1-153 <FUJ>

A:Cross-references: GB:J00264; NID:g186294; PIDN:AA048509.1; PID:g5729676

R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt

Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984

A>Title: T-cell growth factor: complete nucleotide sequence and organization of the g

A:Reference number: A20961; MUID:84170356

A:Accession: A20961

A:Molecule type: DNA

A:Residues: 1-153 <HO2>

A:Cross-references: GB:K02056; NID:g186302; PIDN:AA98792.1; PID:g386819

R:Laabli, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapl

EMBO J. 11, 3897-3904, 1992

A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t (

A:Reference number: S31208; MUID:93010964

A:Accession: S31209

A:Molecule type: mRNA

A:Residues: 11-117 <LAA>

A:Cross-references: EMBL:214955

A>Note: this sequence is shown from the beginning of the fragment to the chromosomal

R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takeoka, C.; Kashima, N.; Yoshimoto, R.; Ham

Nature 302, 305-310, 1983

A>Title: Structure and expression of a cloned cDNA for human interleukin-2.

A:Reference number: A93297; MUID:83167472

A:Accession: A93297

A:Molecule type: mRNA

A:Residues: 1-153 <TRAN>

A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781

A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHRC

R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shima, K.; Fujimoto, K

Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983

A>Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840  
 A:Accession: A90113  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CH>  
 A:Cross-references: GB:J00264; NID:g186294; PIDN:AA048509.1; PID:g5729676  
 A:Experimental source: tonsillar mononuclear cells  
 R:Deves, R.; Plactinck, G.; Chevreure, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau  
 Nucleic Acids Res. 11, 4307-4323, 1983  
 A:Title: Molecular cloning of human Interleukin 2 cDNA and its expression in Escherichia  
 A:Reference number: A93478; MUID:83246551  
 A:Accession: A93478  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <DEV>  
 A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781  
 A:Experimental source: splenocytes  
 R:Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.  
 J. Neurochem. 64, 1928-1936, 1995  
 A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
 A:Reference number: 156518; MUID:95239150  
 A:Accession: 156518  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-152 <E12>  
 A:Cross-references: GB:S77834; NID:g999000  
 A:Accession: 173624  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 5-7, '9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <RES>  
 A:Cross-references: GB:S77833; NID:g999001; PIDN:AD1264.1; PID:g4261964  
 R:Ushino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.  
 Biomed. Res. 6, 197-205, 1985  
 A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
 A:Reference number: 152528  
 A:Accession: 152528  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE2>  
 A:Cross-references: GB:M33109; NID:g186296; PIDN:AA05139.1; PID:g553508  
 R:Steinlist, U.; Durand, D.B.; Bressler, P.; Holdbrook, N.J.; Norris, C.A.; Kamoun, M.;  
 Mol. Cell. Biol. 6, 3042-3049, 1986  
 A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
 A:Reference number: 157603; MUID:87064618  
 A:Accession: 157603  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE3>  
 A:Cross-references: GB:M13879; NID:g186305; PIDN:AA05141.1; PID:g553509  
 R:Wells, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.  
 Biochemistry 27, 6883-6892, 1988  
 A:Title: Structure-activity relationships of recombinant human interleukin 2.  
 A:Reference number: 152401; MUID:89062420  
 A:Accession: 152401  
 A:Contents: recombinant IL-2 and mutants expressed in E. coli  
 A:Accession: 152401  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-21153 <RE4>  
 A:Cross-references: GB:M22005; NID:g186300; PIDN:AA05140.1; PID:g386618  
 R:Robd, R.J.; Kulny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
 A:Title: Amino acid sequence and post-translational modification of human interleukin 2.  
 A:Reference number: A94009; MUID:85038540  
 A:Accession: A94009  
 A:Molecule type: protein  
 A:Residues: 21-153 <ROB>  
 A:Note: disulfide bonds and carbohydrate binding site were determined  
 A:Note: heterogeneity in Jukat-derived IL-2 is primarily due to differences in glycosyl  
 n in lacking 21-Ala (FT-112-B) and 22-Pro (FT-112-B)  
 R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindemaler, W.; Hoppe, J.; Hauser, H.  
 J. Biol. Chem. 264, 17368-17373, 1989  
 A:Title: Expression of human Interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
 de.  
 A:Reference number: A34463; MUID:90008901

A:Accession: A34463  
 A:Molecule type: protein  
 A:Residues: 21-35 <CON>  
 A:Note: the O-linked glycosylation site in recombinant material matched that from hum  
 R:Gribenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.  
 Eur. J. Biochem. 215, 189-197, 1993  
 A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro  
 A:Reference number: S34052; MUID:93345493  
 A:Accession: S34052  
 A:Contents: annotation; glycosylation of variant forms expressed in insect cells  
 C:Genetics:  
 A:Gene: GDB:112  
 A:Cross-references: GDB:119344; OMIM:147680  
 A:Map position: 4q26-4q27  
 A:Introns: 49/3; 69/3; 117/3  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-153/Product: interleukin-2 #status experimental <IL2>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:78-125/Disulfide bonds: #status experimental  
 Query Match 96.7%; Score 147; DB 1; Length 153;  
 Best local similarity 100.0%; Pred. No. 2e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 APTSSSTKTQLOLEHLLDLOMTINGINN 31  
 DB 21 APTSSSTKTQLOLEHLLDLOMTINGINN 50  
 ICG12  
 Interleukin-2 precursor - common gibbon  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Hylobates lar (common gibbon, white-handed gibbon)  
 C:Date: 31-Dec-1991 #sequence\_rev150n 31-Dec-1991 #text\_change 22-Jun-1999  
 C:Accession: A94067; M01849  
 R:Chen, S.J.; Holdbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
 A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c  
 A:Reference number: A94067; MUID:86042650  
 A:Accession: A94067  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CHE>  
 A:Cross-references: GB:M11144; NID:g177014; PIDN:AA35454.1; PID:g177015  
 A:Experimental source: leukemia cell line M1A 14; ATCC TIB 201  
 A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-153/Product: interleukin-2 #status predicted <IL2>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:78-125/Disulfide bonds: #status predicted  
 Query Match 96.7%; Score 147; DB 1; Length 153;  
 Best local similarity 100.0%; Pred. No. 2e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 APTSSSTKTQLOLEHLLDLOMTINGINN 31  
 DB 21 APTSSSTKTQLOLEHLLDLOMTINGINN 50  
 RESULT 3  
 JN0698  
 Interleukin 2 precursor - cat  
 C:Species: Felis silvestris catus (domestic cat)  
 C:Date: 03-Feb-1994 #sequence\_rev150n 03-Feb-1994 #text\_change 16-Jul-1999  
 C:Accession: JN0698  
 R:Cozzl, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.  
 Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
 A:Title: Sequence and functional characterization of feline interleukin 2.  
 A:Reference number: JN0698; MUID:93356765



A:Accession: JN0698  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-154 <CCZ>  
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314  
C:Superfamily: Interleukin-2  
C:Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;  
Best Local Similarity 73.3%; Pred. No. 1.6e-09;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
OY 2 APTSSSTKKTQQLQLEHLLDQMLINGINN 31  
DB 21 APTSSSTKKTQQLQLEHLLDQMLINGINN 50

RESULT 4  
A31278  
Interleukin-2 precursor - rat  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 16-Jul-1999  
C:Accession: A45882; A31278  
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cd  
A:Reference number: A45882; MUID:89339608  
A:Accession: A45882  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MCK>  
A:Cross-references: GB:M2889; NID:g204909; PIDN:AAA41427.1; PID:g204910  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 63.8%; Score 97; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 5.6e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
OY 2 APTSSSTKKTQQLQLEHLLDQMLINGINN 31  
DB 21 APTSSSTKKTQQLQLEHLLDQMLINGINN 50

RESULT 5  
S16241  
Interleukin-2 precursor - pig  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: S16241; S15473  
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.  
A:Reference number: S16241; MUID:91274360  
A:Accession: S16241  
A:Molecule type: mRNA  
A:Residues: 1-154 <GOO>  
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992  
R:Lefevre, F.  
submitted to the EMBL Data Library March 1991  
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain r  
A:Reference number: S15473  
A:Accession: S15473  
A:Molecule type: mRNA  
A:Residues: 1-154 <LEP>  
A:Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-154/Product: Interleukin-2 #status predicted <MAT>

Query Match 63.2%; Score 96; DB 2; Length 154;  
Best Local Similarity 66.7%; Pred. No. 7.8e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
OY 2 APTSSSTKKTQQLQLEHLLDQMLINGINN 31  
DB 21 APTSSSTKKTQQLQLEHLLDQMLINGINN 50

RESULT 6  
S33509  
Interleukin-2 - Mongolian jird  
C:Species: Meriones unguiculatus (Mongolian jird)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S33509  
R:Mal, Z.; Klei, T.; Horohov, D.  
submitted to the EMBL Data Library, October 1992  
A:Description: Cross-species PCR cloning of jird (Meriones unguiculatus) interleukin-  
A:Reference number: S33509  
A:Accession: S33509  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MAL>  
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638  
C:Superfamily: Interleukin-2

Query Match 62.5%; Score 95; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 1.1e-06;  
Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
OY 2 APTSSSTKKTQQLQLEHLLDQMLINGINN 31  
DB 21 APTSSSTKKTQQLQLEHLLDQMLINGINN 50

RESULT 7  
S31391  
Interleukin-2 precursor - horse  
C:Species: Equus caballus (domestic horse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31391  
R:Tavernor, A.S.; Butcher, G.W.  
submitted to the EMBL Data Library, November 1992  
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.  
A:Reference number: S31391  
A:Accession: S31391  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-149 <TAV>  
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077  
C:Superfamily: Interleukin-2

Query Match 60.5%; Score 92; DB 2; Length 149;  
Best Local Similarity 56.7%; Pred. No. 3e-06;  
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
OY 2 APTSSSTKKTQQLQLEHLLDQMLINGINN 31  
DB 21 APTSSSTKKTQQLQLEHLLDQMLINGINN 50

RESULT 8  
S38662  
Interleukin-2 - goat  
C:Species: Capra aegagrus hircus (domestic goat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S38662  
R:Rimstad, E.  
submitted to the EMBL Data Library, November 1993  
A:Description: The molecular cloning and expression of caprine interleukin 2.  
A:Reference number: S38662  
A:Accession: S38662  
A:Status: preliminary



Nucleic Acids Res. 12, 9323-9331, 1984

A>Title: Organization and structure of the mouse Interleukin-2 gene.

A:Reference number: A93550; MUID:85087940

C:Accession: A93550

A:Molecule type: DNA

A:Residues: 1-169 <FUS>

R:Derivative, W.: Simons, G.; Devos, R.; Plaetnick, G.; Remaut, E.; Tavernier, J.; Fiers, W.

Mol. Biol. Rep. 11, 57-61, 1986

A>Title: Cloning and structure of a mouse Interleukin-2 chromosomal gene.

A:Reference number: A54490; MUID:86118396

C:Accession: A54490

A:Molecule type: DNA

A:Residues: 1-169 <DEG>

A:Cross-references: GB:M16760

R:Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.

Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985

A>Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clones

A:Reference number: A94064; MUID:85113172

C:Accession: A94064

A:Molecule type: mRNA

A:Residues: 1-169 <YOK>

A:Cross-references: GB:R02292; NID:g198330; PIDN:AAA39289.1; PID:g309404

R:Kishima, N.; Nishitakaoka, C.; Fujita, T.; Takii, S.; Yamada, G.; Hamuro, J.; Taniguchi, A.

Nature 313, 402-404, 1985

A>Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.

A:Reference number: I48597; MUID:85111148

C:Accession: I48597

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-169 <RES>

A:Cross-references: EMBL:X01772; GB:R02797; NID:g52663; PIDN:CAA2990.1; PID:g758159

C:Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this

C:Genetics: 63/3; 83/3; 132/3

C:Initons: 63/3; 83/3; 132/3

C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

F:1-20/Domin: signal sequence #status predicted <SIG>

F:21-169/Product: interleukin-2 #status predicted <MAT>

F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted

F:92-140/Disulfide bonds: #status predicted

QY 2 APTSST-----KKTOLQLEHLLDQLQNLGNN 31

||||| : || ||||| : : |

Db 21 APTSSSTSSSTAEADOOOOOOOHHLEOLLMDLOELLSWEN 64

RESULT 13

168870

Interleukin 2 - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999

C:Accession: I68870

R:Matasanz, F.; Alcina, A.; Pellicer, A.

Immunogenetics 38, 300-303, 1993

A>Title: Existence of at least five interleukin-2 molecules in different mouse strains.

A:Reference number: I54512; MUID:99307791

C:Accession: I68870

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-60 <RES>

A:Cross-references: GB:I07575; NID:g349515; PIDN:AAA39327.1; PID:g349516

C:Genetics:

A:Gene: Il-2

C:Superfamily: Interleukin-2

Query Match 39.1%; Score 59.5; DB 2; Length 60;

Best Local Similarity 45.5%; Pred. No. 0.072;

Matches 15; Conservative 6; Mismatches 5; Indels 7; Gaps 1;

```

OY      2 APTSSST-----KKTQLQLEHLLDLQMILN 27
          :| |||||
          :| |||||
Db       25 SPTSSTSSSTAFAAQOQQOQQOQQOQQOQHLEQLLDLMDLDELLS 57

RESULT 14
I54512
Interleukin 2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I54512
R:Matesanz, F.; Alcina, A.; Pellicer, A.
Immunogenetics 38, 300-303, 1993
A>Title: Existence of at least five interleukin-2 molecules in different mouse strain
A:Reference number: I54512; MUID:93307791
A:Accession: I54512
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-62 <RES>
A:Cross-references: GB:I07574; NID:g349513; PIDN:AAA39326.1; PID:g349514
C:Genetics:
A:Gene: IL-2
C:Superfamily: Interleukin-2

Query Match           38.5%; Score 58.5; DB 2; Length 62;
Best Local Similarity 42.9%; Pred. No. 0.1;
Matches 15; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

OY      2 APTSSST-----KKTQLQLEHLLDLQMILN 27
          :| |||||
          :| |||||
Db       25 SPTSSTSSSTAFAAQOQQOQQOQQOQHLEQLLDLMDLDELLS 59

RESULT 15
I68871
Interleukin 2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I68871
R:Matesanz, F.; Alcina, A.; Pellicer, A.
Immunogenetics 38, 300-303, 1993
A>Title: Existence of at least five interleukin-2 molecules in different mouse strain
A:Reference number: I54512; MUID:93307791
A:Accession: I68871
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:I07576; NID:g349517; PIDN:AAA39328.1; PID:g349518
C:Genetics:
A:Gene: IL-2
C:Superfamily: Interleukin-2

Query Match           37.8%; Score 57.5; DB 2; Length 72;
Best Local Similarity 35.6%; Pred. No. 0.18;
Matches 16; Conservative 5; Mismatches 5; Indels 19; Gaps 1;

OY      2 APTSSSTKTKTQLQ-----LEHLLDLQMILN 27
          :| |||||
          :| |||||
Db       25 SPTSSTSSSTAFAAQOQQOQQOQQOQQOQHLEQLLDLMDLDELLS 69

Search completed: October 25, 2002, 15:50:06
Job time : 17 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:44:15 ; Search time 11 Seconds

(Without alignments)  
109.119 Million cell updates/sec

Title: US-09-720-828A-2

Sequence: 1 MAPSSSTKRTQLQLEHLLDLQMLNGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	96.7	153	IL2_HUMAN	P01585 homo sapien
2	147	96.7	154	IL2_MACFA	Q29615 macaca fasc
3	147	96.7	154	IL2_MACMU	P51498 macaca mula
4	142	93.4	154	IL2_CERTO	O46649 cercocebus
5	116	76.3	154	IL2_MIRAN	O07885 mirounga an
6	114	75.0	154	IL2_FELCA	O07885 felis silve
7	107.5	70.7	155	IL2_RABIT	O29416 canis famill
8	107	70.4	153	IL2_RABIT	O77620 oryctolagus
9	97	63.8	155	IL2_PIG	P17108 rattus norv
10	96	63.2	154	IL2_PIG	P26891 sus scrofa
11	95	62.5	155	IL2_MERUN	O08081 meriones un
12	92	60.5	149	IL2_HORSE	P37997 equus cabal
13	88	57.9	152	IL2_MOROR	O07513 orcius orc
14	79	52.0	155	IL2_BOVIN	P05016 bos taurus
15	79	52.0	155	IL2_CAPIH	P36835 capra hircu
16	79	52.0	155	IL2_SHEEP	P19114 ovis aries
17	79	52.0	162	IL2_CEREL	P51747 cervus elap
18	64.5	42.4	166	IL2_MOUSE	O08667 mus musculu
19	64	42.1	169	IL2_MOUSE	O04351 mus musculu
20	54	35.5	357	AAAA_EMEIN	P21133 emeticella
21	52	34.2	155	YHCH_HAETN	P44583 haemophilus
22	51	33.6	627	FLUK_BOBBU	P70859 borrelia bu
23	50	32.9	1046	POL_STVAG	P27880 simian immu
24	48	31.6	189	Y064_MERTJA	O60376 methanococc
25	48	31.6	1061	POL_STVAT	P05895 simian immu
26	47.5	31.2	938	PM15_CHLPP	O92883 chlamydia p
27	46	30.3	293	Y347_HELPJT	O92883 chlamydia p
28	46	30.3	627	YHAB_YEAST	P38750 saccharomyc
29	46	30.3	715	LCCL_LACLA	O96138 lactococcus
30	46	30.3	1403	PRO_DROME	O96138 lactococcus
31	45	29.6	1612	DNM1_PARLI	O27746 parascaphila
32	45	29.6	333	ABSC_MTCLE	O05662 mycobacteri
33	45	29.6	715	LCNC_LACLA	O00564 lactococcus

34	45	29.6	870	1	POL_JSRV	P31623 sheep pulmo
35	45	29.6	903	1	MSPI_SCHPO	P87320 schistosach
36	45	29.6	1158	1	ALAI_ARATH	P98204 arabidopsis
37	44.5	29.3	511	1	DOP1_DROME	P41596 drosophila
38	44.5	29.3	741	1	RNSA_HOMAN	O05823 homo sapien
39	44	28.9	81	1	EXYS_PASMU	O9cna0 pasteurella
40	44	28.9	357	1	CAD4_TOBAC	P30359 nicotiana t
41	44	28.9	357	1	CAD9_TOBAC	P30360 nicotiana t
42	44	28.9	368	1	LEU3_NEUCR	P34738 neurospora
43	44	28.9	474	1	SYFA_ARCFU	O28324 archaeglob
44	44	28.9	625	1	XYNA_PIRSP	O12667 pirmyoccs s
45	44	28.9	943	1	YLN5_CAEEL	P34408 caenorhabdi

## ALIGNMENTS

RESULT 1	ID	IL2_HUMAN	STANDARD:	PRT:	153 AA.
AC	P01585	IL2_HUMAN			
BT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)				
DE	(Aldesleukin).				
GN	IL2.				
OS	Homo sapiens (Human), and				
OS	Hylobates lar (Common gibbon).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606, 9580;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RC	MEDLINE-84247353; PubMed-6330695;				
RA	Holbrook N.J., Lieber M., Crabtree G.R.;				
RT	"DNA sequence of the 5' flanking region of the human Interleukin 2				
RT	gene: homologues with adult T-cell leukemia virus.";				
RL	Nucleic Acids Res. 12:5005-5013(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RC	MEDLINE-83167472; PubMed-6403867;				
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,				
RT	Yoshimoto R., Hamuro J.;				
RT	"Structure and expression of a cloned cDNA for human Interleukin-2.";				
RL	Nature 302:305-310(1983).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RC	MEDLINE-84023840; PubMed-6312994;				
RA	Maeda S., Nishino N., Oharu K., Mita S., Nomiya H., Shimada K.,				
RT	Fujimoto K., Teraishi T., Hirano T., Onoue K.;				
RT	"Cloning of Interleukin 2 mRNAs from human tonsils.";				
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RC	MEDLINE-83246551; PubMed-6306584;				
RA	Devos R., Plaetnick G., Cheroutre H., Simons G., Degraeve W.,				
RT	Tavernier J., Remaut E., Fiers W.;				
RT	"Molecular cloning of human Interleukin 2 cDNA and its expression in				
RL	E. coli.";				
RL	Nucleic Acids Res. 11:4307-4323(1983).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RC	MEDLINE-84170356; PubMed-6608729;				
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,				
RT	Wiskocil R.L., Crabtree G.R.;				
RT	"T-cell growth factor: complete nucleotide sequence and organization				
RT	of the gene in normal and malignant cells.";				

RA Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).  
RN [6]  
RC SEQUENCE FROM N.A.  
RX SPECIES-Human;  
RA MEDLINE-84170243; PubMed-6324170;  
RA Fujita T., Takaoka C., Matsui H., Taniguchi T.;  
RA "Structure of the human interleukin 2 gene-";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Human;  
RX MEDLINE-95239150; PubMed-7722480;  
RA Elzenberg O., Faber-Elman A., Lotan M., Schwartz M.;  
RA "Interleukin-2 transcripts in human and rodent brains: possible  
RT expression by astrocytes";  
RL J. Neurochem. 64:1928-1936(1995).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Human; TISSUE-Placenta;  
RX MEDLINE-96422299; PubMed-8824916;  
RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;  
RA "Sequence of interleukin-2 isolated from human placental poly A+ RNA:  
RT possible role in maintenance of fetal allograft.";  
RL Mol. Reprod. Dev. 43:180-186(1996).  
RN [9]  
RP SEQUENCE OF 21-153 FROM N.A.  
RC SPECIES-Human;  
RX MEDLINE-99052420; PubMed-3264184;  
RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;  
RA "Structure-activity relationships of recombinant human interleukin  
RT 2";  
RL Biochemistry 27:6883-6892(1988).  
RN [10]  
RP SEQUENCE OF 1-69 FROM N.A.  
RC SPECIES-Human;  
RX MEDLINE-87064618; PubMed-3491296;  
RA Stebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,  
RA Kamoun M., Kant J.A., Crabtree G.R.;  
RA "Promoter region of interleukin-2 gene undergoes chromatin structure  
RT changes and confers inducibility on chloramphenicol acetyltransferase  
RN Mol. Cell. Biol. 6:3042-3049(1986).  
RN [11]  
RP SEQUENCE OF 1-68 FROM N.A.  
RC SPECIES-Human;  
RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;  
RA "Organization of the DNA regions flanking the human interleukin 2  
RT gene";  
RL Biomed. Res. 6:197-205(1985).  
RN [12]  
RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES-Human;  
RX MEDLINE-85038540; PubMed-6333684;  
RA Robb R.J., Kutry R.M., Panlao M., Morris H.R., Chowdhry V.;  
RA "Amino acid sequence and post-translational modification of human  
RT interleukin 2";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).  
RN [13]  
RP CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES-Human;  
RX MEDLINE-90008901; PubMed-2793860;  
RA Conradt H.S., Nlmtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,  
RA Hauser H.;  
RA "Expression of human interleukin-2 in recombinant baby hamster  
RT kidney, Ltk-, and Chinese hamster ovary cells. Structure of O-linked  
RT carbohydrate chains and their location within the polypeptide.";  
RL J. Biol. Chem. 264:17368-17373(1989).  
RN [14]  
RP SEQUENCE FROM N.A.  
RC SPECIES-H.Iar;  
RX MEDLINE-86042650; PubMed-3877307;  
RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,  
RA Greengard J.S., Crabtree G.R., Lin Y.;

RT "A viral long terminal repeat in the interleukin 2 gene of a cell  
RT line that constitutively produces interleukin 2";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RC SPECIES-Human;  
RX MEDLINE-86070646; PubMed-3500515;  
RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;  
RA "Three-dimensional structure of interleukin-2";  
RL Science 238:1707-1709(1987).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE-92335891; PubMed=1631562;  
RA Bazan J.F.;  
RA "Unraveling the structure of IL-2";  
RL Science 257:410-412(1992).  
RN [17]  
RP RESPONSE TO ABOVE LETTER.  
RA McKay D.B.;  
RL Science 257:412-413(1992).  
RN [18]  
RP STRUCTURE BY NMR.  
RX MEDLINE-92379010; PubMed=1510960;  
RA Molt H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,  
RA Campbell I.D.;  
RA "Secondary structure of human interleukin 2 from 3D heteronuclear NMR  
RT experiments";  
RL Biochemistry 31:7741-7744(1992).  
RN [19]  
RP 3D-STRUCTURE MODELING.  
RX MEDLINE-95111955; PubMed=7529123;  
RA Bamorough P., Hedgecock C.J., Richards W.G.;  
RA "The interleukin-2 and interleukin-4 receptors studied by molecular  
RT modelling";  
RL Structure 2:839-851(1994).  
RN [20]  
RP -I- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS  
CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;p13)  
CC WHICH INVOLVES IL2 AND BCRA.  
CC -I- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used  
CC in patients with renal cell carcinoma or metastatic melanoma.  
CC -I- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
CC -I- DATABASE: NAME-Rad Systems' cytokine source book: IL2;  
CC WWW-"http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyid=206".  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: J00264; AAD48509.1; -  
CC EMBL: X01586; CAA25742.1; -  
CC EMBL: X00564; CAA23827.1; -  
CC EMBL: X00695; CAA25292.1; -  
CC EMBL: K02056; AAA98792.1; -  
CC EMBL: M13879; AAA59141.1; -  
CC EMBL: K03174; AAA35453.1; -  
CC EMBL: S77834; AAD14263.2; -  
CC EMBL: S82692; AAB46883.1; -  
CC EMBL: M22005; AAA59140.1; -  
CC EMBL: M11144; AAA35454.1; -  
CC EMBL: M33199; AAA59139.1; -  
CC EMBL: A14844; CAA01199.1; -  
CC PIR: A01849; ICHU2.  
CC PIR: A94067; ICG12.

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Query Match          96.7%; Score 147; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLINGINN 31
    |||
DB 21 APTSSSTKKTQLEHLLDQMLINGINN 50

RESULT 2
ID IL2_MACFA STANDARD; PRT; 154 AA.
AC 029615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
IL2.
OS Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RL Yabe M., Matsura Y., Tatsumi M.;
   Submitted (Jul-1995) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: D63352; BAA09676.1; -.
CC HSSP: P01585; 31NK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4AA9 CRC64;

Query Match          96.7%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLINGINN 31
    |||
DB 21 APTSSSTKKTQLEHLLDQMLINGINN 50

RESULT 3
IL2_MACMU

```

```

ID IL2_MACMU STANDARD; PRT; 154 AA.
AC P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544; 9545;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RL MEDLINE=9600435; PubMed=7561102;
   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
   "Comparative sequence analysis of cytokine genes from human and
   nonhuman primates.";
   J. Immunol. 155:3946-3954 (1995).
CC -! FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
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CC EMBL: U19847; AAB60400.1; -.
CC EMBL: U19852; AAB6714.1; -.
CC HSSP: P01585; 31NK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17685 MW; 6AEB8480F204BA49 CRC64;

Query Match          96.7%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLINGINN 31
    |||
DB 21 APTSSSTKKTQLEHLLDQMLINGINN 50

RESULT 4
IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
IL2.

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OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cerepithelidae;
OC Cerepithelinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT Comparative sequence analysis of cytokine genes from human and
nonhuman primates.
RL J. Immunol. 155:3946-3954(1995).
CC -I- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U19846; AAB60399.1; -.
DR HSSP: P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR PRODOM: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> R.
SQ SEQUENCE 154 AA; 17754 MW; 9FEB51814204BA48 CRC64;

Query Match 93.4%; Score 142; DB 1; Length 154;
Best Local Similarity 96.7%; Pred. No. 2e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLDDLQMLINGINN 31
DB 21 APTSSSTKKTQLEHLDDLQMLINGINN 50

RESULT 5
IL2_MIRAN STANDARD; PRT; 154 AA.
AC 062641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Mircouga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

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RT *Sequence and characterization of porcine interleukin 2.*;
RL J. Wildt. Dis. 34:81-90(1998).
CC -I- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U79187; AAC12258.1; -.
DR HSSP: P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR PRODOM: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17661 MW; 0C92337AAB1696BB CRC64;

Query Match 76.3%; Score 116; DB 1; Length 154;
Best Local Similarity 73.3%; Pred. No. 1.7e-10;
Matches 22; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLDDLQMLINGINN 31
DB 21 APTSSSTKKTQLEHLDDLQMLINGINN 50

RESULT 6
IL2_FELCA STANDARD; PRT; 154 AA.
AC 007885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356755; PubMed=8352761;
RX Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA Lelf A.R.;
RT *Sequence and functional characterization of feline interleukin 2.*;
RL Blochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Lilman R., Gibbs C., Good R.A., Day N.K.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.

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CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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CC -----  
CC EMBL: L19402; AAA02865.1; -;  
CC EMBL: L25408; AAA51431.1; -;  
CC PIR: JN0698; JN0698.  
CC HSSP: P01585; 3INK.  
CC InterPro: IPR000779; Interleukin-2.  
CC Pfam: PF00715; IL2; 1.  
CC PRINTS: PR00265; INTERLEUKIN2.  
CC ProDom: PD003649; Interleukin-2; 1.  
CC SMART: SM00189; IL2; 1.  
CC PROSITE: PS00424; INTERLEUKIN\_2; 1.  
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
CC T-cell.  
CC FT SIGNAL 1 20 BY SIMILARITY.  
FT CHAIN 21 154 INTERLEUKIN-2.  
FT DISULFID 78 126 BY SIMILARITY.  
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 3 4 KI -> KA (IN REF. 2).  
FT CONFLICT 150 150 F -> I (IN REF. 2).  
SQ SEQUENCE 154 AA; 17653 MW; 2E71E3DB8B65BF CRC64;  
  
Query Match 75.0%; Score 114; DB 1; Length 154;  
Best Local Similarity 73.3%; Pred. No. 3,4e-10;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 APPTSSTKKTQQLQLEHLDDLQMLINGINN 31  
DB 21 APASSSTKKTQQLQLEHLDDLQMLINGVNN 50  
II2\_CANFA STANDARD: PRT: 155 AA.  
AC Q29416; Q28249; -;  
DT 15-JUL-1998 (Rel. 36; Created)  
DT 15-JUL-1998 (Rel. 36; Last sequence update)  
DT 30-MAY-2000 (Rel. 39; Last annotation update)  
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
GN IL2.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;  
RX MEDLINE=95337423; PubMed=7612930;  
RA Dunham S.P., Argyre D.J., Onions D.E.;  
RT "The isolation and sequence of canine Interleukin-2.";  
RL DNA Seq. 5:177-180(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9601696; PubMed=8571541;  
RA Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,  
RA Henthorn P.S.;  
RT "A single nucleotide insertion in the canine Interleukin-2 receptor  
RT gamma chain results in X-linked severe combined immunodeficiency  
RT disease.";  
RL Vet. Immunol. Immunopathol. 47:203-213(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BEAGLE; TISSUE=Spleen;  
RX MEDLINE=95347614; PubMed=7622066;

RA Knapp D.W., Williams J.S., Andrisani O.M.;  
RT "Cloning of the canine Interleukin-2-encoding cDNA.";  
RL Gene 159:281-282(1995).  
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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CC -----  
CC EMBL: D30710; BAA06378.1; -;  
CC EMBL: U28141; AAA68969.1; -;  
CC EMBL: U11689; AAA75360.1; -;  
CC HSSP: P01585; 3INK.  
CC InterPro: IPR000779; Interleukin-2.  
CC Pfam: PF00715; IL2; 1.  
CC PRINTS: PR00265; INTERLEUKIN2.  
CC ProDom: PD003649; Interleukin-2; 1.  
CC SMART: SM00189; IL2; 1.  
CC PROSITE: PS00424; INTERLEUKIN\_2; 1.  
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
CC T-cell.  
CC FT SIGNAL 1 20 BY SIMILARITY.  
FT CHAIN 21 155 INTERLEUKIN-2.  
FT CARBOHYD 24 124 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 79 127 BY SIMILARITY.  
FT CONFLICT 4 4 M -> I (IN REF. 3).  
FT CONFLICT 37 37 Q -> R (IN REF. 3).  
FT CONFLICT 151 151 F -> Y (IN REF. 3).  
FT CONFLICT 154 154 L -> M (IN REF. 3).  
SQ SEQUENCE 155 AA; 17668 MW; D123E48B8B7F4AC1D CRC64;  
  
Query Match 70.7%; Score 107.5; DB 1; Length 155;  
Best Local Similarity 71.0%; Pred. No. 3,3e-09;  
Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;  
  
QY 2 APPTSSTKKTQQLQLEHLDDLQMLINGINN 31  
DB 21 APSSSTKKTQQLQLEHLDDLQMLINGVNN 51  
II2\_RABIT STANDARD: PRT: 153 AA.  
AC Q77520; -;  
DT 15-JUL-1999 (Rel. 38; Created)  
DT 15-JUL-1999 (Rel. 38; Last sequence update)  
DT 16-OCT-2001 (Rel. 40; Last annotation update)  
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
GN IL2.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9906;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph node;  
RA Kerr P.J., Lei S., Hardy C., Perkins H.D.;  
RT "Complete cDNA sequence of rabbit Interleukin-2.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE

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 DR EMBL; X56750; CAA40071.1; -  
 DR EMBL; X58428; CAA41350.1; -  
 DR EMBL; AB041935; BAB16110.1; -  
 DR PIR; S15473; S15473.  
 DR PIR; S16241; S16241.  
 DR HSSP; P01585; 31NK.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 T-cell.  
 KM SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.  
 FT CAROXYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.  
 SQ SEQUENCE 154 AA; 17401 MW; F3B95543D4A3D3E1 CRC64;  
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 Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
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 OY 2 APTSSSTKTQLEHLLDMLINGINN 31  
 DB 21 APTSSSTKTQLEHLLDMLINGINN 50  
 IL2\_MERUN  
 ID IL2\_MERUN STANDARD; PRT; 155 AA.  
 AC 008081;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Meriones unguiculatus (Mongolian jird).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxId=10047;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=94174702; PubMed=8128610;  
 RA Mei Z., Kousoulas K.G., Horchov D.W., Klei T.R.;  
 RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)  
 Interleukin-2 cDNA and its expression in COS-7 cells.";  
 RT Vet. Immunol. Immunopathol. 40:63-71(1994).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
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 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 DR EMBL; X68779; CAA48679.1; -  
 DR PIR; S33509; S33509.  
 DR HSSP; P01585; 31NK.

DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;  
 T-cell.  
 KM SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 155 INTERLEUKIN-2.  
 FT CAROXYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT DISULFID 78 126 BY SIMILARITY.  
 SQ SEQUENCE 155 AA; 17602 MW; D0F74AA1A393CDA CRC64;  
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 Best Local Similarity 66.7%; Pred. No. 2.5e-07;  
 Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
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 OY 2 APTSSSTKTQLEHLLDMLINGINN 31  
 DB 21 APTSSSTKTQLEHLLDMLINGINN 50  
 IL2\_HORSE  
 ID IL2\_HORSE STANDARD; PRT; 149 AA.  
 AC P37997;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxId=9796;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=94160538; PubMed=8116217;  
 RA Vandergilte E.V., Horchov D.W.;  
 RT "Molecular cloning and expression of equine interleukin 2.";  
 RT Vet. Immunol. Immunopathol. 39:395-406(1993).  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA Tavernor A.S., Allen W.R., Butcher G.W.;  
 RT Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
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 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
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 DR EMBL; L06009; AAA20134.1; -  
 DR EMBL; X69393; CAA49190.1; -  
 DR PIR; S31391; S31391.  
 DR HSSP; P01385; 31NK.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;

```

KW T-cell. 1 20 BY SIMILARITY.
FT SIGNAL 21 149 INTERLEUKIN-2.
FT CHAIN 78 121 BY SIMILARITY.
FT DISULFID 23 23 O-LINKED (GLYNAC. . .) (BY SIMILARITY).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 3 R -> K (IN REF. 2).
FT CONFLICT 8 8 S -> A (IN REF. 2).
FT CONFLICT 59 59 I -> M (IN REF. 2).
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT CONFLICT 128 128 E -> G (IN REF. 2).
FT CONFLICT 145 145 I -> F (IN REF. 2).
FT CONFLICT 148 148 L -> M (IN REF. 2).
SQ SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64;

Query Match 60.5%; Score 92; DB 1; Length 149;
Best Local Similarity 56.7%; Pred. No. 6.9e-07;
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLIDLIOMIINGINN 31
Db 21 APTSSSTKTKTQLEHLIDLIOMIINGINN 50

RESULT 13
IL2_ORCOR STANDARD; PRT; 152 AA.
AC 097513;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF) (Fragment).
GN IL2.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RA Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;
RT "Isolation and expression of the interleukin-2 gene from the killer whale, Orcinus orca."
RL Mar. Mamm. Sci. 14:531-543(1998).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
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CC EMBL: AF009570; AAD01426.1; -.
CC HSSP: P01585; IIRL.
CC InterPro: IPR00779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KV T-cell.
FT SIGNAL 1 20 BY SIMILARITY.

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FT CHAIN 21 >152 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GLYNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308F91821ECB764 CRC64;

Query Match 57.9%; Score 88; DB 1; Length 152;
Best Local Similarity 60.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLIDLIOMIINGINN 31
Db 21 APTSSSTKTKTQLEHLIDLIOMIINGINN 50

RESULT 14
IL2_BOVIN STANDARD; PRT; 155 AA.
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205869; PubMed=3517854;
RA Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D., Gillis S., Cosman D., Baker P.E.;
RT "Cloning, sequence, and expression of bovine interleukin 2."
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205870; PubMed=3486415;
RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D., Barr P.J., Magnuson N.S., Magnuson J.A.;
RT "Molecular cloning of a functional bovine interleukin 2 cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Thymus;
RA Anlikeeva N.N., Vinogradova T.V., Votoshin O.N.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
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CC EMBL: M12791; AAA30586.1; -.
CC EMBL: M13204; AAA21143.1; ALT_INTF.
CC EMBL: X17201; CAA35062.1; -.
CC EMBL: X52687; CAA36912.1; -.
CC HSSP: P01585; 31NK.
CC InterPro: IPR00779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.

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DR SMART: SM00189; IL2: 1.
DR PROSITE: PS00424; INTERLEUKIN_2: 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
FT SIGNAL 1 20
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match
Best Local Similarity 53.3%; Score 79; DB 1; Length 155;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDLQMLINGINN 31
DB 21 APTSSSTGNTMKVSKSLLDLDLLEKYN 50

RESULT 15
IL2_CAPRI STANDARD: PRT: 155 AA.
AC p36835; p79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rumsdall E.;
RA Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RL Beyer J.C.; Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL: X76063; CAA53664.1; -
CC EMBL: U34274; AAB38527.1; -
CC DR EMBL: U34274; AAB38527.1; -
CC DR PIR: S38662; S38662.
CC DR HSP: P01585; SINK.
CC DR InterPro: IPR000779; Interleukin-2.
CC DR Pfam: PF00715; IL2: 1.
CC DR PRINTS: PR00265; INTERLEUKIN2.
CC DR PRODOM: PD003649; Interleukin-2; 1.
CC DR SMART: SM00189; IL2: 1.
CC DR PROSITE: PS00424; INTERLEUKIN_2: 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.

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FT CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
FT DISULFID 79 127 BY SIMILARITY.
FT CONFLICT 3 5 RMO -> QTP (IN REF. 2).
FT CONFLICT 22 22 P -> T (IN REF. 2).
FT CONFLICT 30 30 T -> P (IN REF. 2).
FT CONFLICT 51 51 L -> P (IN REF. 2).
FT CONFLICT 71 71 D -> A (IN REF. 2).
FT CONFLICT 89 89 D -> E (IN REF. 2).
FT CONFLICT 99 99 R -> L (IN REF. 2).
FT CONFLICT 107 113 YMASLKG -> SMDNIKR (IN REF. 2).
FT CONFLICT 140 140 Q -> L (IN REF. 2).
FT CONFLICT 144 144 T -> I (IN REF. 2).
FT CONFLICT 154 154 L -> M (IN REF. 2).
SQ SEQUENCE 155 AA; 17703 MW; 90022D9BB6A6F78DE CRC64;

Query Match
Best Local Similarity 53.3%; Score 79; DB 1; Length 155;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDLQMLINGINN 31
DB 21 APTSSSTGNTMKVSKSLLDLDLLEKYN 50

Search completed: October 25, 2002, 15:48:51
Job time : 13 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 25, 2002, 15:44:41 ; Search time 25 Seconds  
(without alignments)  
214.514 Million cell updates/sec

Title: US-09-720-828A-2  
Perfect score: 152  
Sequence: 1 MAPSSSTKTKTQLEHLLDQMLNGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*  
15: SP:virus:\*  
16: SP:bacteriaph:\*  
17: SP:archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	150	4	Q9C001 homo sapien
2	145	95.4	154	6	Q9X538 papio hamad
3	135.5	89.1	156	4	Q13169 homo sapien
4	134	88.2	139	4	Q16334 homo sapien
5	108.5	71.4	155	6	Q9X783 halichoerus
6	107.5	70.7	66	6	Q9B74 canis fami
7	107	70.4	79	6	Q9TV12 canis fami
8	106	69.7	133	6	Q9M2R9 oryctolagus
9	106	69.7	155	11	Q923T2 sigmodon hi
10	103	67.8	138	11	Q70329 mesocricetu
11	91	59.9	91	4	Q9UCF5 homo sapien
12	83	54.6	154	6	Q9X784 delphinape
13	82	53.9	152	11	Q88210 capra porce
14	79	52.0	69	6	Q9GJ84 ovis aries
15	79	52.0	155	6	Q9GL83 capra hircu
16	79	52.0	155	6	Q95MP4 ovis aries

17	79	52.0	155	6	Q95KP3 bubalus bub
18	69	45.4	39	6	Q9BG73 canis fami
19	69	45.4	150	11	P70291 mus musculu
20	69	45.4	169	11	Q9GUS8 mus musculu
21	67	44.1	150	11	P70294 mus musculu
22	65.5	43.1	155	11	P70292 mus musculu
23	62.5	41.1	159	11	P70293 mus musculu
24	52	34.2	116	6	Q29138 trichechus
25	52	34.2	737	16	Q9K7G5 vibrio chol
26	51	33.6	304	16	Q930K5 rhizobium m
27	51	33.6	457	5	Q9N7P5 strongyloce
28	50	32.9	365	16	P71599 mycobacteri
29	50	32.9	579	4	Q9PT93 homo sapien
30	50	32.9	667	11	Q924H2 mus musculu
31	50	32.9	746	4	Q96RNS homo sapien
32	50	32.9	748	4	Q96CT0 homo sapien
33	50	32.9	1454	4	Q60244 homo sapien
34	50	32.9	1454	4	Q9UNB3 homo sapien
35	50	32.9	3175	12	Q91DM2 equine arte
36	49	32.2	230	16	Q9KMS6 vibrio chol
37	49	32.2	458	5	O15996 hemientrot
38	49	32.2	543	16	Q9KSF8 arabidopsis
39	49	32.2	651	10	Q22042 caenorhabdi
40	49	32.2	1130	5	Q20417 caenorhabdi
41	48.5	31.9	240	5	Q20417 caenorhabdi
42	48	31.6	441	2	Q928V0 listeria mo
43	48	31.6	441	16	Q928V0 listeria mo
44	48	31.6	595	5	Q9VFW6 dirosophila
45	47.5	31.2	155	3	Q74353 schizosacch

## ALIGNMENTS

RESULT 1	Q9C001	PRELIMINARY:	PRT:	150 AA.
AC	Q9C001:	01-JUN-2001 (TREMBLrel. 17, Created)		
DP	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	INTERLEUKIN-2 (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20545237; Pubmed-11093171;			
RA	Malestanz F., Delgado C., Fresno M., Alcina A.;			
RT	"Allelic selection of human IL-2 gene."			
RI	Eur. J. Immunol. 30:3516-3521(2000).			
DR	EMBL: AF228636; AAC53575.1; -.			
DR	HSSE: P01585; 31NK.			
DR	InterPro: IPR000779; Interleukin-2.			
DR	Pfam: PF00715; IL2; 1.			
DR	PRINTS: PR00265; INTERLEUKIN2.			
DR	PRODOM: PD003649; Interleukin-2; 1.			
DR	SMART: SM00189; IL2; 1.			
DR	PROSITE: PS00424; INTERLEUKIN_2; 1.			
PT	NON-TRP 150			
SQ	SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;			
Query Match	96.7%;	Score 147;	DB 4;	Length 150;
Best Local Similarity	100.0%;	Pred. No. 1.6e-14;		
Matches 30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2	APTSSSTKTKTQLEHLLDQMLNGINN 31		
DB	21	APTSSSTKTKTQLEHLLDQMLNGINN 50		
RESULT 2				





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RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL: AF072871: AAd0848.1: -.
DR HSSP: P01585: 31NK.
DR InterPro: IPR000779: Interleukin-2.
DR Pfam: PF00715: IL2: 1.
DR PRINTS: PR00265: INTERLEUKIN2.
DR PRODOM: PD003649: Interleukin-2: 1.
DR SMART: SM00189: IL2: 1.
DR PROSITE: PS00424: INTERLEUKIN_2: 1.
SQ SEQUENCE 155 AA: 17860 MW: F18F449AC672241A CRC64:

Query Match
Best Local Similarity 71.4%: Score 108.5; DB 6; Length 155;
Matches 23; Conservative 5; Mismatches 2; Indels 1; Gaps 1:

OY 2 AP-TSSSTKKTQLEHLDDLQMLINGINN 31
DB 21 APTSSSTKETQQLLEQLLDLRLINGVNN 51

RESULT 6
O9BG74 PRELIMINARY: PRT: 66 AA.
AC O9BG74:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE INTERLEUKIN 2 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID-9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD:
RA Markus S., Greene A., Baumgaertner W.;
RT *Expression of canine Interleukin-2 mRNA in concanavalin A-stimulated
RT canine lymphocytes.*
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF33117: AAK01437.1: -.
DR HSSP: P01585: 11RL.
DR InterPro: IPR000779: Interleukin-2.
DR PRINTS: PR00265: INTERLEUKIN2.
DR PRODOM: PD003649: Interleukin-2: 1.
DR SMART: SM00189: IL2: 1.
DR NON_TER 1
FT NON_TER 66
SQ SEQUENCE 66 AA: 7389 MW: 22A893F79DA2AE47 CRC64:

Query Match
Best Local Similarity 70.7%: Score 107.5; DB 6; Length 66;
Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1:

OY 2 AP-TSSSTKKTQLEHLDDLQMLINGINN 31
DB 14 APTSSSTKETQQLLEQLLDLRLINGVNN 44

RESULT 7
O9TV12 PRELIMINARY: PRT: 79 AA.
AC O9TV12:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE INTERLEUKIN-2 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID-9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
```

```

RT "Cloning and sequencing of canine IL-2."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF091131: AAD46989.1: -.
DR HSSP: P01585: 11RL.
DR InterPro: IPR000779: Interleukin-2.
DR Pfam: PF00715: IL2: 1.
DR PRINTS: PR00265: INTERLEUKIN2.
DR PRODOM: PD003649: Interleukin-2: 1.
DR SMART: SM00189: IL2: 1.
DR PROSITE: PS00424: INTERLEUKIN_2: 1.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA: 9087 MW: 83079BF8FA559BD CRC64:

Query Match
Best Local Similarity 70.4%: Score 107; DB 6; Length 79;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0:

OY 4 TSSSTKKTQLEHLDDLQMLINGINN 31
DB 7 TSSSTKETQQLLEQLLDLRLINGVNN 34

RESULT 8
O9MZR9 PRELIMINARY: PRT: 133 AA.
AC O9MZR9:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE INTERLEUKIN 2 VARIANT IL2DELTA2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID-9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN, LYMPH NODE:
RA MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT *The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).*
RL Cytokine 12:555-565(2000).
DR EMBL: AF169168: AAF6652.1: -.
DR HSSP: P01585: 31NK.
DR InterPro: IPR000779: Interleukin-2.
DR Pfam: PF00715: IL2: 1.
DR PRODOM: PD003649: Interleukin-2: 1.
DR SMART: SM00189: IL2: 1.
DR PROSITE: PS00424: INTERLEUKIN_2: 1.
SQ SEQUENCE 133 AA: 14748 MW: 0D54758C190B5655 CRC64:

Query Match
Best Local Similarity 69.7%: Score 106; DB 6; Length 133;
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0:

OY 2 APTSSSTKKTQLEHLDDLQMLINGINN 30
DB 21 APTSSSTKETQQLLEQLLDLRLINGVNN 49

RESULT 9
O9Z3T2 PRELIMINARY: PRT: 155 AA.
AC O9Z3T2:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE INTERLEUKIN 2.
OS Sigmodon hispidus (hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
```

OC Sigmund.  
 NCBI\_TaxID=42415;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Darinell M.R., Plenevea L.M., Langley R.J., Blanco J.C., Prince G.A.;  
 RT Cloning, expression and purification of cotton fat IL-2."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF398549; AAK94012.1; -  
 SO SEQUENCE 155 AA; 17627 MW; ACADBA865E993291 CRC64;

Query Match 69.7%; Score 106; DB 11; Length 155;  
 Best Local Similarity 73.3%; Pred. No. 2.8e-06;  
 Matches 22; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDQMLINGINN 31  
 |||||||:|:| |||||:|:| |  
 Db 21 APTSSSTKKTQLEHLLDQMLINGINN 50

## RESULT 10

070329 PRELIMINARY; PRT; 138 AA.

AC 070329;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE INTERLEUKIN-2 (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NCBI\_TaxID=10036;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-SPLEEN;  
 MEDLINE=98234044; PubMed=9573100;  
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RT leishmaniasis."  
 RL Infect. Immun. 66:2135-2142(1998).  
 DR EMBL: AF046212; AAC40097.1; -  
 DR HSP: P01585; 31NK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS: PR00265; INTERLEUKIN2.  
 DR PRODOM: PD003649; Interleukin-2; 1.  
 DR SMART: SM00189; IL2; 1.  
 DR PROSITE: PS00424; INTERLEUKIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SO SEQUENCE 138 AA; 15739 MW; 35103295B670779 CRC64;

Query Match 67.8%; Score 103; DB 11; Length 138;  
 Best Local Similarity 73.3%; Pred. No. 7.1e-08;  
 Matches 22; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDQMLINGINN 31  
 |||||||:|:| |||||:|:| |  
 Db 14 APTSSSTKKTQLEHLLDQMLINGINN 43

## RESULT 11

090CF5 PRELIMINARY; PRT; 23 AA.

AC 090CF5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE INTERLEUKIN 2 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=93289963; PubMed=8512072;  
 RA Mullner S., Karbe-Thonges B., Tripler D.;  
 RT "Charge heterogeneity of insulin fusion proteins expressed in  
 RT Escherichia coli is not due to proteolytic degradation."  
 RL Anal. Biochem. 210:366-373(1993)  
 SO SEQUENCE 23 AA; 2637 MW; 40B64C6875C021F CRC64;

Query Match 59.9%; Score 91; DB 4; Length 23;  
 Best Local Similarity 90.5%; Pred. No. 7.7e-07;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 TSSSTKKTQLEHLLDQMLINGINN 24  
 |||||||:|:| |||||:|:| |  
 Db 3 TSSSTKKTQLEHLLDQMLINGINN 23

## RESULT 12

09XT84 PRELIMINARY; PRT; 154 AA.

AC 09XT84;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN 2.  
 OS Delphinapterus leucas (Beluga whale).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
 OC Monodontidae; Delphinapterus.  
 NCBI\_TaxID=9749;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99221046; PubMed=10206205;  
 RA St-Laurent G., Beliveau C., Archambault D.;  
 RT "Molecular cloning and phylogenetic analysis of beluga whale  
 RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin  
 RT 2."  
 RL Vet. Immunol. Immunopathol. 67:385-394(1999).  
 DR EMBL: AF072870; AAD40847.1; -  
 DR HSP: P01585; 31NK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS: PR00265; INTERLEUKIN2.  
 DR PRODOM: PD003649; Interleukin-2; 1.  
 DR SMART: SM00189; IL2; 1.  
 DR PROSITE: PS00424; INTERLEUKIN\_2; 1.  
 SO SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 54.6%; Score 83; DB 6; Length 154;  
 Best Local Similarity 56.7%; Pred. No. 8.7e-05;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDQMLINGINN 31  
 |||||||:|:| |||||:|:| |  
 Db 21 APTSSSTKKTQLEHLLDQMLINGINN 50

## RESULT 13

088210 PRELIMINARY; PRT; 152 AA.

AC 088210;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE INTERLEUKIN 2 PRECURSOR.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10141;  
 RN (1)  
 RP SEQUENCE FROM N.A.

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RC TISSUE-SPLEEN;
RA Takeyoshi M., Iwata H., Inoue T.;
RT "Guinea pig Interleukin 2(IL-2) precursor.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010993; BAA31346.1; -.
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD03649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 152 AA; 17271 MW; CA7AC08C186DD1FA CRC64;

Query Match
Best Local Similarity 53.98; Score 82; DB 11; Length 152;
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
DB 21 APTSSSPKOTDRLELLRLDQTLLEGVTS 50

RESULT 14
Q9GJR4 PRELIMINARY: PRT: 69 AA.
ID 09GJR4.
AC 09GJR4.
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE INTERLEUKIN 2 PRECURSOR (FRAGMENT).
GN IL-2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHEEP 2, AND SHEEP 1;
RA Lueken G., Pritzenberg E.-M., Hiendleder S., Erhardt G.;
RT "A single strand conformation polymorphism in the ovine interleukin 2
  (IL-2) gene.";
RL J. Anim. Sci. 0:0-0(2000).
DR EMBL: AF215687; AAG43986.1; -.
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD03649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT NON_TER.
SQ SEQUENCE 69 AA; 7711 MW; B8768C238B34D1AE CRC64;

Query Match
Best Local Similarity 52.0%; Score 79; DB 6; Length 69;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
DB 21 APTSSSTGTMTKEVKSLLDQLLLEKVN 50

RESULT 15
Q9GLB3 PRELIMINARY: PRT: 155 AA.
ID 09GLB3.
AC 09GLB3.
DT 01-MAR-2001 (Tremblrel. 16, Created)

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DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE INTERLEUKIN 2.
GN IL-2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying O.H., Li X.R., Pan J.Y.;
RT "Cloning of the goat IL-2 gene and its expression in E.coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307018; AAG28783.1; -.
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD03649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 155 AA; 17605 MW; EEBB2DE18F5469AA CRC64;

Query Match
Best Local Similarity 52.0%; Score 79; DB 6; Length 155;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
DB 21 APTSSSTGTMTKEVKSLLDQLLLEKVN 50

Search completed: October 25, 2002, 15:49:24
Job time : 28 secs

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